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- (71) Applicant (*for all designated States except US*): **MOLECULAR DYNAMICS, INC.** [US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **PENN, Sharron, G.** [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). **HANZEL, David, K.** [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). **CHEN, Wen-sheng** [CN/US]; 210 Easy Street #25, Mountain View, CA

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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.



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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_HEART.txt, created
25 24 January 2001, having 20,186,946 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins -- known or suspected -- about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences -- that is, those accessible through isolation of mRNA -- are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods
25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

30

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
35 invention also provides apparatus for verifying the

expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful
5 for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in
10 sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a
15 sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at
20 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof
30 wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981
35 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding
5 a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in
10 accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or
15 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.
20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in
25 accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid
30 probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those
35 skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a
5 single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to
15 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in
20 accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each
25 probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from
30 genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said
35 probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a single exon
microarray in accordance with the first aspect of the
invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
gene.

20 In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 9,981 - 19,771,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
of SEQ ID NOS.: 1 - 9,980.

30 In a further aspect, the invention provides
peptides comprising an amino acid sequence translated from
the DNA fragments, said amino acid sequences comprising SEQ
ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

 As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence
15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted
25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.
30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
35 expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records
5 corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector
10 sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence
15 identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence.
20 Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in
25 information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the
30 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than
35 human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any
5 given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb,
10 and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate
15 pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according
20 to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be
25 in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were
30 static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence,
35 either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

5 One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further
10 described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of
15 the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

 If query 20 incorporates multiple criteria, such
20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

25 If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query
30 20 can be generated that takes into account the initial negative result.

 When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired
35 analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent
5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu
10 repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by
20 proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases
25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or
30 codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the
35 specific nucleotide references to one that is unrecognized

by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

5 Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

 Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

25 Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified
30 within the genomic sequence.

 As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a
10 given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset
15 thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene
20 prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5%
25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among
30 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset
35 thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

10 For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
35 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger

fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as
5 PRIMER3 (available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of
10 genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can
15 be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of
20 primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The
25 common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming
30 sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been
35 obtained, or a closely related species, and can

conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in
5 Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs
10 are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could
15 potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally
20 surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

25 After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

30 Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass,
35 although other materials, such as amorphous or crystalline

silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, 5 polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly 10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more 15 typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying 20 nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, 25 Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. 30 For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of 35 background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or
5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose
10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the
15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed
20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in
25 Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography
30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at
35 least 1000, typically at least 2000, preferably 5000 and

upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin
5 from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the
10 homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message
15 polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein
20 as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material.
25 Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

30 In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60,
35 70 or 80% or more of individual exon-including probes

disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding
5 region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression
10 measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a
15 single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the
20 average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-
25 spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95
30 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the
35 probes in the genome-derived single exon microarrays of the

present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

5 After the physical substrate is prepared, experimental verification of predicted function is performed.

 In a preferred embodiment of the present invention, where the function sought to be identified in
10 genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

 Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query – including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and

last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs
5 (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with
10 the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

15 Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display
20 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the
25 probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As
30 noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of
35 bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked
10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the
25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for
30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute
35 expression (signal intensity) can be expressed using

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay
5 is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing
10 gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene
15 predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as
20 white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of
25 sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

30

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present
35 invention rapidly identify and confirm the expression of

portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from
5 previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic
10 acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human
15 genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of
20 skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a
25 significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as
30 causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in
35 the United States and other developed countries. In

developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD
5 each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will
10 continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a
15 severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another
25 risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or
30 lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

35 The literature is replete with evidence for

genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL),
5 that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

10 As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

15 Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm
20 Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular
25 risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of
30 hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic
35 kidney disease, medullary thyroid cancer, pheochromocytoma,

and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable
5 antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both genetic and environmental components. The recent search
10 for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor
15 receptor-2, and α -adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell
20 sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major
25 locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major
30 locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene,
35 with gender and age dependence. They also suggested that a

single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on
5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367
10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than
15 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone,
20 encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for
25 cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or
30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular
35 block, familial sinus node disease, progressive cardiac

conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

10 For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been
15 linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3.
20 Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations
25 in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated
30 cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

35 In addition, cardiomyopathy can also be caused by

mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with
5 reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

10 Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-
15 p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the
20 His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000
25 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott
30 et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United
35 States. Twenty percent of infants with congenital heart

disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the
5 second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao
10 syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects
15 have been identified. For example, Greenberg et al., Am. J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al.,
20 Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several
25 genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those
30 located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who
35 underwent fluorescence in situ hybridization (FISH) testing

with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

5 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known
10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

 In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with
20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

 In another approach, the genome-derived single
25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel
30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

35 The utility is specific to the probe; at

sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel *et al.* and Maniatis *et al.* — each probe reports the level of expression of message specifically containing that ORF.

5 It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

10 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
15 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
20 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
25 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
30 that are currently available for achieving these utilities.

 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
35 for surveying gene expression in the human.

Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 5 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 10 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for 15 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 20 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

25 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell 35 Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
46(3):425-8 (1999)), in drug discovery screens (see, for
5 example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
Expression Profile Analysis of Human Breast Cancer
10 Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
appreciated that even those probes that show no change in
15 expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
failure of the agent to change a gene's expression level is
20 evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
lead compound discovery or in subsequent screening of lead
25 compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

WO 99/58720 provides methods for quantifying the
30 relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
percentage of the individual gene expression measurements
35 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena *et al.*

5 The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

 The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
10 sufficient to perform a hybridization reaction.

 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
15 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
20 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

 Usefully, however, such probes are provided in a
25 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
30 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
35 to be provided in a form suitable for amplification, the

range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

10 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
20 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
25 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
30 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a
35 hybridization reaction in which the probe is not first

bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

5 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
10 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

15 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be
20 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency
25 conditions.

 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
30 poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
35 stringency conditions can usefully be aqueous hybridization

at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in
5 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of
10 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

15 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are
20 maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly
25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further
30 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
35 sequence complementary to those described herein above and

below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
5 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
10 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

15 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
20 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
25 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

30 When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
35 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be

25 used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open
5 reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to
10 Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range
15 of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

20 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by
25 all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window
30 were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

35

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method
5 approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support
10 substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF
15 was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was
20 commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to
25 add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon
30 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR®
35 green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 \pm 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
25 finding algorithms.

 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent
5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was
10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using
15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of
20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
25 produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of
30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt
35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
5 "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate
10 of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes
15 expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

20 The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

25 FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all
30 sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the
35 ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large
5 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA
10 library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to
15 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic
20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific
25 gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies,
30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two
35 sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
35

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai *et al.*, *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

 The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

20 Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

 The mean and standard deviation of the modified control spot populations are calculated.

 The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria:
1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 9,980) and probe exon (SEQ ID NOs.: 9,981 – 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

. . (a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human heart.

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
442	10386	20209	4.41				
871	10797	20647	17.08				
1029	10947		2.14				
1280	11188	21039	7.97				
1597	11501	21361	1.87				
1619	11523	21381	4.97				
1694	11596	21467	1.01				
1715	11616	21485	0.95				
1721	11622	21491	7.45				
1848	11744	21620	0.98				
1935	11830	21713	3.03				
2119	12008	21907	2.62				
2233	12118	22020	2.34				
3149	13074	22875	3.7				
3403	13320	23121	1.52				
3471	13387	23192	8.97				
3513	13429		0.87				
3607	13521	23309	0.99				
4102	14002	23781	1.71				
4164	14064	23838	5.94				
4184	14084	23858	0.89				
4184	14084	23859	0.89				
4242	14141		1.03				
4730	14616	24402	1.76				
4779	14663		0.78				
4976	14851	24617	5.08				
4988	14863	24629	2.07				
5217	15140	24834	1.92				
5217	15140	24835	1.92				
5328	15248		5				
5436	15356		5.89				
5483	15248		4.9				
5509	15427	25490	2.9				
5688	19451	25678	1.6				

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5690	15599	25700	1.41				
5863	15769		1.84				
6382	16244	26404	1.61				
6382	16244	26405	1.61				
6697	16577	26769	1.29				
6942	16820	27012	1.3				
7494	17364	27569	3.58				
7684	17534	27758	1.26				
8070	17961		3.7				
8219	19472	28355	2.31				
8390	18266		2.84				
8686	18555	28840	2.91				
8757	17906	28150	1.73				
8757	17906	28151	1.73				
8792	18606		2.19				
9464	19094		1.62				
9760	19280	25230	2.11				
5691	15600	25701	13.31	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6669	16549	26745	1.54	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
7955	17805	28046	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
7955	17805	28047	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2631	12499	22399	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22390	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2893	12820	22612	5.91	9.4E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
7206	17083	27271	2.97	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5239	15163	24932	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24933	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5678	15587	25687	5.51	8.9E+00	BE971806.1	EST_HUMAN	801851038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754	25871	1.71	8.7E+00	AB019798.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5848	15754	25872	1.71	8.7E+00	AB019798.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
433	10378	20199	1.76	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
7439	16452	26642	3.68	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (sec2a)
8509	18381		2.31	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6346	16209		2.07	7.6E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
6868	16747	26940	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6868	16747	26941	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	26531	2.58	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
7085	16662	27155	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
7085	16662	27156	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2947	12874	22672	4.2	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17386		8.48	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8090	18577	28860	3.26	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
7735	17585	27809	2.98	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8575	18443	28712	1.85	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
6818	16697	26889	2.72	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7925	17775	28015	1.3	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
6614	16494	26680	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:291860 5'
6614	16494	26681	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:291860 5'
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
7277	17154		1.47	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8
7863	17713	27957	3.82	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
7796	17646	27881	2.1	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7796	17646	27882	2.1	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18344		2.17	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C5C3.05C
7296	17172	27372	8.32	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
7616	17467	27686	1.44	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
							Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
5828	15833	25956	7.16	5.9E+00	AF155142.1	NT	
3479	13395		0.81	5.8E+00	7631557	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8770	17919	28166	2.44	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
8769	17918	28165	2.65	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8967	18773		1.94	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
6593	16473		1.62	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
7769	17619	27849	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
7769	17619	27850	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4875	14661	24354	1.54	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6710	16990		4.04	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8899	18708	29003	3.21	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
7655	17505	27730	1.21	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
7959	17809	28050	3.06	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
8610	18477	28749	10.53	5.0E+00	Z83960.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
3972	13879		9.43	4.9E+00	AF185255.1	NT	Enuice australis histone H3 (H3) gene, partial cds
6970	16847		5.01	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
286	10251	20071	2.03	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
287	10251	20071	1.92	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3236	13160	22958	4.01	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6576	16434	26617	1.48	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
8881	18693	28986	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3003	12931	22723	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3003	12931	22724	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
5764	15671		1.55	4.4E+00	X13414.1	NT	Murine I gene for MHC class II(a) associated invariant chain
6398	16259	26420	2.01	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
8235	18116	28368	7.49	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5387	15306		2.92	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
6060	16043	26188	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6060	16043	26187	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
7182	17059	27249	5.45	4.2E+00	AI809013.1	EST_HUMAN	wf67g03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6517	16376	26553	7.65	4.1E+00	Q23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6577	16435	26618	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6577	16435	26619	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6617	16497	26584	2.95	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
7576	17427	27641	2.31	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC. 62 Homo sapiens cDNA clone IMAGE:4333209 5'
8259	18139		2.89	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
8339	18216		12.46	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC. 71 Homo sapiens cDNA clone IMAGE:3909051 5'
9672	19231	25241	1.86	4.1E+00	P47876	SWISSPROT	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF-BINDING PROTEIN 1)
6266	16131	26285	1.37	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8768	17917	28164	2.17	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
8835	18648	28834	3.34	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
8835	18648	28835	3.34	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
3459	13375	23181	3.89	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4226	14124		0.99	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5471	15391	25454	2.47	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5471	15391	25455	2.47	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6108	16002	26140	4.46	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
6355	16218	26379	4.68	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6840	16719	26913	2.32	3.9E+00	X65885.1	NT	Xlaevis mRNA for M4 muscarinic receptor
8695	17879	28120	3.09	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
8715	18532	28816	5.58	3.9E+00	AA661489.1	EST_HUMAN	nr18a12.s1 NCL_OGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2588	12459		2.4	3.8E+00	AE001862.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6911	16789	26982	1.18	3.8E+00	D44725.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3936	13846	23622	10.09	3.7E+00	AL161539.2	NT	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
8730	18536	28872	2.13	3.7E+00	BF669279.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
8730	18536	28873	2.13	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC. 56 Homo sapiens cDNA clone IMAGE:4277748 5'
578	10516	20322	2.1	3.6E+00	AV761055.1	EST_HUMAN	602120551F1 NIH_MGC. 56 Homo sapiens cDNA clone IMAGE:4277748 5'
7022	16899	27090	3.66	3.6E+00	AE004447.1	NT	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
7022	16899	27091	3.66	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
7022	16899	27091	3.66	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		3.78	3.6E+00	M96795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
3209	13133	22934	1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1496	11400	21260	3.57	3.4E+00	AF284577.1	NT	Brassica napus RPB5d mRNA, complete cds
2532	12406	22298	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6354	16217	26378	2.41	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17739	27982	3.17	3.4E+00	AF013187.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8818	18631	28919	1.92	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5036	14908	24679	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14908	24680	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
492	10435	20248	1.39	3.2E+00	X96422.1	NT	D.reio zp-50 POU gene
3938	10435	20248	0.79	3.2E+00	X96422.1	NT	D.reio zp-50 POU gene
5439	15369	25415	2.68	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5439	15369	25416	2.68	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5808	15713	25825	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5808	15713	25826	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6569	16427	26609	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6569	16427	26610	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7221	17098		6.33	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
7491	17361	27567	1.17	3.2E+00	M36383.1	NT	S.cerevisiae threonine deaminase (LLV1) gene, complete cds
7837	17687	27932	1.69	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for glutaryl cyclase C, complete cds
9089	18863		4.32	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5582	15497	25574	2.42	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7000	16577	27067	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7000	16577	27068	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7334	17238		3.8	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
7920	17770	28009	4.78	3.1E+00	P49865	SWISSPROT	DEOXYHYPUSE SYNTHASE (DHS)
							GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8759	17908		3.78	3.1E+00	P33515	SWISSPROT	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
8774	18591		3.35	3.1E+00	S56660.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2807	12737	22535	1.06	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5273	15195	24970	1.63	3.0E+00	X53096.1	NT	S.aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6245	16111		9.5	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45	3.0E+00	X67838.1	NT	B.napus DNA for mycosinase
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28501	6.51	3.0E+00	F51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28502	6.51	3.0E+00	F51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
1964	11858	21747	2.56	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
6129	15876	26112	1.63	2.9E+00	Z36879.1	NT	F. pringii gdsPA gene for P-protein of the glycine cleavage system
6282	16146	26300	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6282	16146	26301	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6410	16271	26433	5.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11346	21212	5.79	2.8E+00	AF165398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1615	11519		3.12	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188	26350	4.78	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
230	10199	20012	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
230	10199	20013	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5408	15327	25377	1.75	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00	BE063527.1	EST_HUMAN	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
4576	14467	24253	4.35	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15324	25373	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5405	15324	25374	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
							Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
6533	16391		5.42	2.6E+00	AF235502.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
6896	18376	26767	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
6896	16576	26768	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
7567	17418	27634	2.95	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7927	17777		1.52	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19649		2.31	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1448	11353	21216	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1448	11353	21217	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5552	15468	25537	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5552	15468	25538	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25537	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25538	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6561	16419	26598	1.34	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7284	17141	27334	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9086	18831		2.26	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
9086	12907	22707	0.86	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4816	14699	24485	7.62	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5657	15599	25664	4.19	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
6733	16613	26802	2.14	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6733	16613	26803	2.14	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6780	16659		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
7026	16903		1.71	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7125	17002	27104	9.45	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17621	27653	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7771	17621	27654	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7820	17670	27911	2.18	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
7881	17731		6.49	2.4E+00	P03099	SWISSPROT	XYLOLOSE KINASE (XYLOKINASE)
7914	17764	28002	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7914	17764	28003	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
8428	18302	28558	1.77	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 76 degrees: glpPFD operon and downstream
8665	18554	28839	2.52	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1233	11140	20992	9.36	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4031	13934		1.28	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6408	16269	26431	2.22	2.3E+00	6978564	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6479	19766		2.3	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	16431	26613	1.53	2.3E+00	XG0265.1	NT	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
7289	17165	27364	1.81	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
8988	18793	29083	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8988	18793	29084	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9304	19002	25333	4	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
9936	19405		1.37	2.3E+00	AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5276	15198	24973	10.08	2.2E+00	O88307	SW/ISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5276	15198	24974	10.08	2.2E+00	O88307	SW/ISSPROT	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
5696	15605	25707	9.06	2.2E+00	BE250383.1	EST_HUMAN	MINOR VIRION STRUCTURAL PROTEIN MU-2
5835	15741	25853	3.3	2.2E+00	Q00335	SW/ISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
5978	15882	26005	2.89	2.2E+00	P51459	SW/ISSPROT	igf5b02.st NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3'
6155	15113		3.14	2.2E+00	AA594574.1	EST_HUMAN	z005g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
6486	16344	26514	51.56	2.2E+00	AA449012.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
7381	17250		11.83	2.2E+00	BE741678.1	EST_HUMAN	TRANSPOSON TY1 PROTEIN A
7518	19468		2.1	2.2E+00	Q04706	SW/ISSPROT	qm68b03.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1893965 3'
7783	17633	27865	1.56	2.2E+00	AI290373.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7783	17633	27866	1.56	2.2E+00	AI290373.1	EST_HUMAN	qm68b03.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1893965 3'
7812	17662	27902	2.28	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7975	17825	28066	2.88	2.2E+00	AF183416.1	NT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
8739	17888	28132	4.5	2.2E+00	P07911	SW/ISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
8889	18700	28995	4.67	2.2E+00	P10407	SW/ISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
557	12670	20304	6.81	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3539	13455		1.19	2.1E+00	AW449366.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6074	16057	26206	3.72	2.1E+00	O70159	SW/ISSPROT	UH-B13-akt-s-08-0-JL.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6195	15955	26087	4.7	2.1E+00	N29575.1	EST_HUMAN	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6948	16826		1.99	2.1E+00	AL123630.1	EST_HUMAN	w48at0.s1 Soares_melanocyte_2NbIM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
1178	11089	20934	1.23	2.0E+00	AF180527.1	NT	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
							AU123630 NT2RM2 Homo sapiens cDNA clone NT2RV2000671 5'
							Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1178	11089	20935	1.23	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1313	11219	21076	1.43	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Nat-1 (K-ATPase beta 1 subunit mRNA, complete cds
1557	11462		3.13	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYL TRANSFERASE SPB1
2102	11991	21890	4.6	2.0E+00	Z78279.1	NT	R.novgicus mRNA for collagen alpha1 type I
2102	11991	21891	4.6	2.0E+00	Z78279.1	NT	R.novgicus mRNA for collagen alpha1 type I
4011	13917	23692	2.09	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb.X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4011	13917	23693	2.09	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb.X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
6678	16558	26751	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26752	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26753	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7170	17047	27237	3.3	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
9629	19613	24998	6.81	2.0E+00	5834943	NT	Gallus gallus mitochondrion, complete genome
5437	15357	25412	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5437	15357	25413	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6047	15950		2.27	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
6927	16805	26999	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6927	16805	27000	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7032	16909		3.36	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT014-010900-323-h12 MT0114 Homo sapiens cDNA
7156	17033		1.86	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
3054	12981	22773	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	13009	22799	4.48	1.8E+00	U04355.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3082	13009	22800	4.48	1.8E+00	U04355.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5577	15492		2.22	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	15620	25723	1.9	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6043	15946	26078	1.3	1.8E+00	BF306552.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7140	17017	27210	2.09	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
7293	17169	27369	1.21	1.8E+00	R31042.1	EST_HUMAN	yf72c08.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:136278 5'
7899	17749		3.29	1.8E+00	AF111849.1	NT	Homo sapiens PRO0550 mRNA, complete cds
8998	18801		3.76	1.8E+00	P36062	SWISSPROT	HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CIM5YTA3 INTERGENIC REGION

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9428	19584		4.01	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9504	19119		2.4	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
9988	19429		1.34	1.8E+00	BF316805.1	EST_HUMAN	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135686 5'
1092	11008	20849	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013	3.25	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202	22101	1.02	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4356	14252	24037	0.84	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369	25424	1.48	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5448	15369	25425	1.48	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5664	15575	25673	3.58	1.7E+00	Q911TR	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7014	16891		1.29	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
7282	19487	27355	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
7282	19487	27356	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
8874	18686	28977	1.78	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9384	19044	25306	1.37	1.7E+00	AI678443.1	EST_HUMAN	tu82407.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.1f
9660	19351	25185	2.26	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element;
1989	11892	21775	16.73	1.6E+00	AF199339.1	NT	qf50b01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.1 L1
1997	11891	21783	3.61	1.6E+00	AF077374.1	NT	repetitive element;
2003	11896	21788	1.96	1.6E+00	Y11344.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2238	12122		1.48	1.6E+00	X96373.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2931	12858	22658	2.52	1.6E+00	W58426.1	EST_HUMAN	Mus musculus ST6GalNAcII gene, exon 2
3946	13854		5.14	1.6E+00	BF570077.1	EST_HUMAN	B.napus gene encoding endo-polygalacturonase
4255	14154	23928	1.44	1.6E+00	AF155827.1	NT	zcd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4255	14154	23929	1.44	1.6E+00	AF155827.1	NT	gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
5016	14890	24657	3.14	1.6E+00	Y11344.1	NT	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
5016	14890	24658	3.14	1.6E+00	Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5558	15474	25546	2.19	1.6E+00	L04808.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
6296	16190	26317	2.64	1.6E+00	BE997267.1	EST_HUMAN	Mus musculus ST6GalNAcII gene, exon 2
						NT	Mus musculus ST6GalNAcII gene, exon 2
						NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
						EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6681	16561		1.21	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
6881	16760	26958	3.56	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
7444	19465	26646	1.3	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
7444	19465	26647	1.3	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
7611	17462	27679	1.29	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hmcDNA library/Homo sapiens cDNA clone ph6b6_19/1TV
7852	17702	27946	1.25	1.6E+00	AW835844.1	EST_HUMAN	QV4-L T0016-090200-100-d07 LT0016 Homo sapiens cDNA
7852	17702	27947	1.25	1.6E+00	AW835844.1	EST_HUMAN	QV4-L T0016-090200-100-d07 LT0016 Homo sapiens cDNA
8217	15520	25601	5.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
8944	18752	29047	3.25	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9902	19379		1.65	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
30	10017	19812	4.29	1.5E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
605	10541		1.79	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2359	12239	22135	2.46	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2468	12344	22237	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3099	12239	22135	2.22	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.82	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5856	15762	25880	2.71	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain T1NB Homo sapiens cDNA clone IMAGE:31693 5'
6230	16096		1.42	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
6250	16116	26268	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6250	16116	26269	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7971	17521	27747	7.56	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
7782	17632		1.71	1.5E+00	BF376754.1	EST_HUMAN	602035771F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
7856	17706	27951	1.96	1.5E+00	AA017693.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
7856	17706	27952	1.96	1.5E+00	AA017693.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
8702	18520	28802	3.91	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfrb1) Homo sapiens cDNA clone IMAGE:361306 3'
8828	18641		10.73	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and tRNA-Phe pseudogene
9223	18946		1.5	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
9596	19178		2.89	1.5E+00	AL445055.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9690	19243		1.42	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA
27	10014	19808	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27	10014	19809	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	12116		0.95	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2286	12169		9.38	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2634	12501	22394	1.63	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12608	22500	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	12608	22501	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12962	22755	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3034	12962	22756	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3291	13213		0.87	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4162	14062	23835	1.09	1.4E+00	AW900455.1	EST_HUMAN	CVO-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4162	14062	23836	1.09	1.4E+00	AW900455.1	EST_HUMAN	CVO-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4482	14376		1.53	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5137	15004		0.8	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5301	15222	25026	1.51	1.4E+00	AW054976.1	EST_HUMAN	w45907.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5394	15313		5.17	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
5796	15702	25812	2.39	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5802	19766		4.9	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5860	15766	25884	2.71	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
5860	15766	25885	2.71	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	16181	26341	1.86	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7107	16984		5.21	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7266	17133	27326	1.88	1.4E+00	R20459.1	EST_HUMAN	y33f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
7303	17179	27381	3.37	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301290-012-f05 BT0313 Homo sapiens cDNA
8420	18294	28548	1.94	1.4E+00	AA195528.1	EST_HUMAN	zr36e09.r1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element
8556	18426	28695	4.97	1.4E+00	AB006682.1	NT	MER22 repetitive element
8709	18526	28808	5.15	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APECED mRNA for AIRE-1, complete cds
8709	18526	28809	5.15	1.4E+00	BE962107.2	EST_HUMAN	60'665184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8727	18593	28867	2.68	1.4E+00	U30790.1	NT	60'665184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8727	18593	28868	2.68	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9221	19604		1.34	1.4E+00	AL161500.2	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
558	10498		1.67	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-ribose dehydrogenase
559	10510	20659	2.74	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1113	11028		16.5	1.3E+00	Y19213.1	NT	Homo sapiens putative psilHbA pseudogene for hair keratin, exons 2 to 7
1275	11183	21033	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1275	11183	21034	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	11241		1.62	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1593	11497		2.09	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2196	12083		2.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPB genes for mannose-binding lectin-associated serine protease (MASP)
2503	12378		2.19	1.3E+00	BE966735.2	EST_HUMAN	and MASP-related protein, complete cds
2909	12835	22632	1.12	1.3E+00	6755621	NT	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3547	13463	23258	1.03	1.3E+00	AF016494.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spnat1), mRNA
4502	12835	22632	0.82	1.3E+00	6755621	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55) synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4964	14839	24607	0.98	1.3E+00	AJ252087.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spnat1), mRNA
4964	14839	24608	0.98	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25674	7.76	1.3E+00	AW362834.1	EST_HUMAN	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25675	7.76	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-408 CT0289 Homo sapiens cDNA
5864	15770	25889	1.33	1.3E+00	M33496.1	NT	PMO-CT0289-291199-004-408 CT0289 Homo sapiens cDNA
6828	16707	26901	1.25	1.3E+00	AJ009912.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6917	16795	26988	3.06	1.3E+00	BE963379.2	EST_HUMAN	Sus scrofa plp gene
7054	16931		1.55	1.3E+00	6910247	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
7480	17350		5.44	1.3E+00	AF042084.1	NT	Homo sapiens GL004 protein (GL004), mRNA
7487	17357	27560	2.31	1.3E+00	X72019.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase 2 gene, complete cds
7487	17357	27561	2.31	1.3E+00	X72019.1	NT	S.alba pht-1 mRNA for photolase
7574	17425	27639	1.45	1.3E+00	O00754	SWISSPROT	S.alba pht-1 mRNA for photolase
7620	17471	27690	1.27	1.3E+00	A1927629.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
7675	17525	27751	4.9	1.3E+00	BE963379.2	EST_HUMAN	wo85a07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
7663	17716	27961	1.0	1.3E+00	AE004392.1	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
7874	17724	27968	1.39	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
8078	17969		4.3	1.3E+00	Q14117	SWISSPROT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
8277	18157	28398	2.34	1.3E+00	P25299	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
							MRNA 3'-END PROCESSING PROTEIN RNA15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8299	18178	28424	2.23	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
8646	18510		1.81	1.3E+00	AW274791.1	EST_HUMAN	XP09503.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739808 3'
8826	18639	28923	2.82	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8895	18705	28999	2.71	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
9362	19033		2.35	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel (Kir2.2 (KCNJ12) gene, complete cds
9533	19139	25283	3.24	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCL CGAP_Brm67 Homo sapiens cDNA clone IMAGE:418452 5'
9644	19499		2.68	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
634	10571	20384	8.14	1.2E+00	AA676246.1	EST_HUMAN	z122d08.s1 Soares fetal liver spleen.1NFLS.S1 Homo sapiens cDNA clone IMAGE:431535 3'
806	10735	20578	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
806	10735	20579	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
806	10735	20580	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
800	10786		2.19	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1145	11058	20901	5.63	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1963	11857	21746	1.05	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22789	0.95	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22851	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	13053	22852	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13172		2.9	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3312	13233		0.99	1.2E+00	M81779.1	NT	G.gallus 1-cadherin mRNA, complete cds
3650	13564	23350	7.28	1.2E+00	U75802.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3904	13814	23598	1.49	1.2E+00	BF373570.1	EST_HUMAN	MR0-F10175-050900-203-g06_1 F10175 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4298	14196	23981	1.39	1.2E+00	6980951	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA
4371	14267		1.64	1.2E+00	M87060.1	NT	Rattus rattus cardiac A23 gene, exons 1-23
4422	14316	24102	1.26	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	14354	24145	1.82	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4485	14379		5.44	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4584	13233		0.94	1.2E+00	M81779.1	NT	G.gallus 1-cadherin mRNA, complete cds
5409	15329	25379	1.96	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c06 ST0191 Homo sapiens cDNA
5739	15647	25753	2.47	1.2E+00	X74885.1	NT	D.hydrel ay1 repeat cluster DNA, fragment D
5769	15676	25783	3.28	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5798	15704	25815	1.87	1.2E+00	X89084.1	NT	C. glutamicum pia gene and ackA gene
5798	15704	25816	1.87	1.2E+00	X89084.1	NT	C. glutamicum pia gene and ackA gene
5823	15729	25841	32.83	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
5918	15823	25949	1.82	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6139	15936	26121	2.55	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6369	19463	26392	1.9	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
6508	16367	26544	2.4	1.2E+00	X74207.1	NT	L. lactis pyrD and pyrF genes
6984	16861	27055	3.45	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7218	17095	27285	1.74	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
7407	17274	27480	3.08	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27601	1.8	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
7711	17581	27786	3.28	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
8653	18542	28826	2.03	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
8689	18576		23.47	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
8752	17901	28145	4.87	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
9114	18877	28787	2.5	1.2E+00	AF065398.1	NT	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds
9330	19572	25067	15.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9349	19025		1.49	1.2E+00	AF001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
456	10400	20217	1.13	1.1E+00	D85980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1726	11627	21496	1.39	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1857	11753	21628	0.92	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-alk-f-02-O-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3288	13209	23009	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	13209	23010	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	13358	23165	0.93	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3510	13426		1.26	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	13447	23244	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3657	13571	23357	1.16	1.1E+00	AE003886.1	NT	SW:P531_HUMAN_Q12888 P53-BINDING PROTEIN 53BP1 ;
3657	13571	23358	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3678	13592	23378	17.81	1.1E+00	5729757	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3862	13773	23565	0.99	1.1E+00	8922641	NT	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA
4122	14022		5.89	1.1E+00	5835331	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4860	14740	24520	1.18	1.1E+00	L23195.1	NT	R. uniconis complete mitochondrial genome
4921	14800	24573	2.92	1.1E+00	U13466.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
						NT	African swine fever virus, complete genome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4999	14874	24638	1.16	1.1E+00	X78425.1	NT	E faecalis pbb5 gene
5249	15172	24945	1.57	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5449	15370	25426	12.04	1.1E+00	BE60184.1	EST_HUMAN	601662776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825635 3'
5460	15380	25440	1.29	1.1E+00	A1138582.1	EST_HUMAN	qd85c03.xt Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6422	16283	26444	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	16283	26445	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6435	16296	26458	7.53	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6728	16508	26789	3.22	1.1E+00	BF983996.1	EST_HUMAN	602082592F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246028 5'
7688	17508	27733	1.65	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
7715	17565	27791	4.39	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27815	20.08	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
8043	17934	28182	2.65	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
8090	17981		3.41	1.1E+00	AF068942.1	NT	Klebsoridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8447	13426		5.73	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
8450	18323	28581	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8450	18323	28582	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8662	18551	28835	4.73	1.1E+00	AI809699.1	EST_HUMAN	wf76e11.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
9300	18989		4	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19056	26310	2.13	1.1E+00	AF216896.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
9523	19570		1.54	1.1E+00	AF234169.1	NT	Dichostelium discoideum isopentenyl pyrophosphate isomerase (Dip1) mRNA, complete cds
92	10077		3.49	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
108	10089	19904	1.14	1.0E+00	D89425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
412	10358		2.16	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
562	10502	20308	1.14	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
661	10595	20413	4.51	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
663	10597		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1364	12592		1.04	1.0E+00	X80416.1	NT	V.carteri Algal-CAM mRNA
1722	11623	21492	1.32	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein precursor, complete cds
2435	12312	22208	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2651	12518	22408	1.09	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Naiip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naiip-rs3) genes, complete cds
2846	12774	22561	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	12774	22562	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	12865		0.99	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3162	13087	22891	1.17	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element;
3327	13247		0.81	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3548	10077		1.15	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3627	13541	23328	1.44	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
3978	13885	23660	0.86	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4178	14078		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4815	14698		0.88	1.0E+00	U75741.1	NT	Taenia ovis 45W antigen (ToW4) gene, complete cds
4951	14828		0.88	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5139	15006	24777	0.87	1.0E+00	AJ223978.1	NT	Bacillus subtilis 42.7kB DNA fragment from ywsA to ywqA
5228	15152	24919	2.49	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5568	15484	25557	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5568	15484	25558	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5719	15628	25729	4.82	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
5720	15627	25730	1.39	1.0E+00	AW452782.1	EST_HUMAN	U1-H-B13-ax-d-09-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
5908	15814	25939	2.21	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6417	16279		8.43	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6537	16395	26574	1.34	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
6546	16404	26583	5.99	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:888791 3'
6641	16521	26713	1.71	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6641	16521	26714	1.71	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6734	14828		1.38	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	16740	26932	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6861	16740	26933	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6967	19496		2.01	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-a08 HT0229 Homo sapiens cDNA
7094	16941	27133	1.9	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
7339	17207	27405	1.76	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
7460	17320	27526	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7460	17320	27527	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7544	17395	27607	2.03	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
7546	17397	27609	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
7546	17397	27610	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
7916	17796	28005	2.83	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWCo4 5'
7985	17835	28075	17.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7985	17835	28076	17.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
9193	18928		2.05	1.0E+00	P16306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
9513	19126		1.51	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
9859	19350		1.67	1.0E+00	AB040950.1	NT	Homo sapiens mRNA for KIAA1517 protein, partial cds
1553	11458	21315	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOGO III mRNA, complete cds
1553	11458	21316	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOGO III mRNA, complete cds
2598	12467	22360	0.9	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	13458		1.18	9.9E-01	AF174565.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5461	15381	25441	9.22	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
7336	17204		1.38	9.9E-01	U65667.1	NT	Lycopodium esculentum putative M1 copy 1 nematode-resistance gene
7510	17298		2.43	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
8097	17988	28237	2.92	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
512	10454	20265	2.32	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13644	23429	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3732	13644	23430	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6272	16137	26292	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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6272	16137	26293	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8362	18239	28487	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8362	18239	28488	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
9408	19061		1.62	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
5106	14974		1.01	9.7E-01	AI660384.1	EST_HUMAN	we62e04.X1 Soares thymus NHFTn Homo sapiens cDNA clone IMAGE:2345094 3'
6248	16114	26266	2.37	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
6962	16830	27023	1.86	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
6954	16832	27025	1.74	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mot) and restriction endonuclease (res)
8510	18382		4.52	9.7E-01	BF511209.1	EST_HUMAN	U1-H-B14-act-e-07-0-U1 s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
9956	19419		1.39	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4337	14234	24016	6.8	9.6E-01	AF107925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	9.6E-01	AF107925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4955	14251	24036	1.3	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5083	14953	24729	0.92	9.6E-01	7682375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5517	15435	25498	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5517	15435	25499	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6890	16769		1.37	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
8808	18622	28912	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG06 5'
8808	18622	28913	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG06 5'
9709	19646	24989	1.52	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3715	13627	23410	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3715	13627	23411	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
7266	17143	27336	1.17	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-01-1-b02 CT0295 Homo sapiens cDNA
3165	13090		3.37	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3181	13108		1.67	9.4E-01	AF080595.1	NT	Piripinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8354	19029		1.64	9.4E-01	BE781251.1	EST_HUMAN	U1-466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
9708	19564		1.43	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1700	11601		1.11	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2594	12464	22357	1.13	9.3E-01	BE071172.1	EST_HUMAN	RC5.BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
3949	13857	23630	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	13857	23631	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5155	15022		1.54	9.3E-01	AF075615.1	NT	Equus caballus microsatellite LEX013
5434	15354	25410	1.62	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5482	15402	25465	3.84	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
6701	16581	26771	1.88	9.3E-01	AA847040.1	EST_HUMAN	oe09503.s1 NC1 CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9822	19325		1.56	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl.34 mRNA, complete cds
9954	19418		1.38	9.3E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
3201	13125	22930	3.04	9.2E-01	BE822702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5643	15556	25649	4.23	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
7618	17489	27688	1.38	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
7890	17740	27983	3.63	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
7952	17802	28041	1.73	9.2E-01	BF593251.1	EST_HUMAN	7668e06.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3678219 3' similar to SW:NU5M_TRYBB
8950	18767	29059	1.85	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
9006	18809	29101	2.01	9.2E-01	BF680047.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2077	11987		1.43	9.1E-01	8923056	NT	602154769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295896 5'
3169	13094	22898	0.97	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20043 (FLJ20048), mRNA
3169	13094	22899	0.97	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
4310	14207	23991	0.86	9.1E-01	U68172.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
5919	15824	25950	2.92	9.1E-01	Q61704	SWISSPROT	Rattus norvegicus mucin (MUC2) gene, partial cds
6472	16331	26498	15.99	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6551	16409	26587	2.2	9.1E-01	U72995.1	NT	ob71908.s1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
9445	19641		30.05	9.1E-01	AF050113.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3170	13095	22900	0.89	9.0E-01	7661625	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4282	14181	23959	2.37	9.0E-01	AF099810.1	NT	Homo sapiens DKFZP964M2423 protein (DKFZP964M2423), mRNA
4945	14821	24589	0.82	9.0E-01	AF017729.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
6388	16250		1.45	9.0E-01	D38621.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
						NT	Xenopus laevis gene for aldolase, complete cds

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5494	15413	25476	2.08	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5786	15392		1.32	8.9E-01	X60096.1	NT	Rabbit MHC fragment RLA-DF DNA
8990	18794	29085	3.47	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
9285	18987		4.74	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4442	14336	24126	3.28	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
8430	18304	28560	2.98	8.8E-01	Z28337.1	NT	Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1
9108	19722		1.75	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
457	10401	20218	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2353	12233	22130	1.09	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2845	12773	22560	4.64	8.7E-01	AA595863.1	EST_HUMAN	nm05f1.1 s1 NCL CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
4938	14816		2.51	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
7613	17464	27681	1.45	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
8206	18090	28343	5.47	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
8970	18776	29067	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8970	18776	29068	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
9488	19534		2.78	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
466	10409		1.66	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
840	10767	20618	3.62	8.6E-01	W69089.1	EST_HUMAN	zd44a03.r1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2224	12109	22012	1.01	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3568	13482	23273	0.81	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3730	13642	23427	1.29	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5595	15509	25586	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5595	15509	25587	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6030	15934	26065	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6030	15934	26066	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6626	16506		1.52	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
6443	16304	26469	2.75	8.5E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7924	17774	28013	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
7924	17774	28014	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9430	19643		2.52	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
9436	19076		2.63	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
9683	19238	25243	1.29	8.5E-01	AB030818.1	NT	Mus musculus mper1 gene for period1, complete cds
4108	14008	23785	0.84	8.4E-01	AF143509.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5378	19443	25145	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5378	19443	25146	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571		3.13	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
724	10656	20486	2.31	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3056	12983	22774	2.64	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3739	13651	23434	1	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3930	13839	23619	3.11	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4917	14796	24570	1.12	8.3E-01	U48916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
4917	14796	24571	1.12	8.3E-01	U48916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24570	0.95	8.3E-01	U48916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24571	0.95	8.3E-01	U48916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5222	15145	24839	2.13	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7573	17424		4.2	8.3E-01	A1791952.1	EST_HUMAN	nm01f12.v5 NCL CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
7822	17672	27914	1.23	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
7867	17717	27962	3.1	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
8062	17953	28204	2.46	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
8076	17967		2.46	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
8623	18488	28760	2.03	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHLT) gene, exon 5
2006	11898	21789	2.99	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2043	11934		1.51	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2646	12513		1.14	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
5046	14917	24691	1	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6122	16016	26154	3.26	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-061199-037-e01 HT0243 Homo sapiens cDNA
6309	19462	26330	3.58	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7788	17638	27871	1.53	8.2E-01	AF052659.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
7937	17787	28028	6.66	8.2E-01	IQ9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7937	17787	28029	6.66	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8009	18717	29011	2.81	8.2E-01	L10127.1	NT	Moluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8966	18772	29064	6	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8971	18777	29069	6.65	8.2E-01	H87398.1	EST_HUMAN	yr14d02.r1 Soares_placenta_8to9weeks_2NbpH8to9W Homo sapiens cDNA clone IMAGE:262195 5'
9451	19083	25284	1.73	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2731	12593		1.29	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3412	13329	23130	2.81	8.1E-01	AF050566.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3412	13329	23131	2.81	8.1E-01	AF050566.1	NT	Homo sapiens MHC class 1 region
5992	15897	26020	2.49	8.1E-01	Q13491	SWISSPROT	Homo sapiens MHC class 1 region
5992	15897	26021	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28879	1.94	8.1E-01	BE938558.1	EST_HUMAN	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28880	1.94	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
9166	18909	25343	1.84	8.1E-01	AE001711.1	NT	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
170	10142		3.02	8.0E-01	AJ271510.1	NT	Thermococcus maritima section 23 of 136 of the complete genome
285	10250	20070	3.76	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
1980	11884		1.83	8.0E-01	BF630962.1	EST_HUMAN	Bos taurus tub and rif genes
3039	12967	22761	2.73	8.0E-01	AF127897.1	NT	602072473F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215091 5'
3273	13194	22893	1.14	8.0E-01	AB006193.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3643	13557		1.8	8.0E-01	AL162758.2	NT	Mus musculus gene for oviductal glycoprotein, complete cds
4432	14327	24115	5.65	8.0E-01	X83739.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
6661	16541		2.84	8.0E-01	AW901489.1	EST_HUMAN	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
446	10390	20211	3.78	7.9E-01	D11476.1	NT	RCO-TN1012-270300-021-h06 NN1012 Homo sapiens cDNA
698	10631		1.16	7.9E-01	AE002130.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1587	11491		65.97	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1634	11538		1.37	7.9E-01	U32739.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
2216	12102	22006	5.24	7.9E-01	AB004816.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2217	12103	22007	2.29	7.9E-01	AF130459.1	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
3472	13388	23193	2.75	7.9E-01	AF228664.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
4204	14103		0.92	7.9E-01	BE263812.1	EST_HUMAN	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4508	14401	24188	1.02	7.9E-01	6753745	NT	60192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4508	14401	24189	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5075	14945	24720	0.84	7.9E-01	Z47210.1	NT	Mus musculus dexB, cap3A, cap3B and cap3C genes and orfs
5075	14945	24721	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5084	14954		1.01	7.9E-01	M29930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6721	16501	26790	2.43	7.9E-01	X90996.1	NT	P. salivum GR gene
7504	17373	27582	4.78	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
7781	17631	27864	3.95	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249		2.36	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8543	18415	28682	2.48	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
858	10784		1.75	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041, normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2229	12114	22016	3.2	7.8E-01	AW959597.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4603	14491	24278	0.79	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5698	15607	25709	2.32	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
7323	17199	27399	1.27	7.8E-01	Y10159.1	NT	D. discoideum racGAP gene
9424	19623		1.42	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
138	10112	19932	6.33	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	10641		1.85	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IIBeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II>
2680	12545	22436	2.8	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3313	13234		0.8	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylglucosaminyltransferase 7 (GalNac-T7) (GALNAC-T7), mRNA
3549	13484	23259	4.45	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4297	14195	23979	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4297	14195	23980	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5415	15335	25386	1.44	7.7E-01	P16553	SWISSPROT	RAFINOSE INVERTASE (INVERTASE)
5415	15335	25387	1.44	7.7E-01	P16553	SWISSPROT	RAFINOSE INVERTASE (INVERTASE)
5626	15541	25630	1.95	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9212	10112	19932	2.6	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	19004		6.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5710	15018	25720	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5710	15618	25721	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds

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6699	16579	26770	1.41	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
6726	16606	26796	2.04	7.6E-01	6857752	NT	Mus musculus activin (Activ-pending), mRNA
6726	16606	26797	2.04	7.6E-01	6857752	NT	Mus musculus activin (Activ-pending), mRNA
7184	17061	27252	1.28	7.6E-01	6753877	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
7347	17215	27414	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27415	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
8664	18553	28837	2.31	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8664	18553	28838	2.31	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8948	18756		4.81	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18850		2.74	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
502	10444		1.52	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21, segment HS21C101
569	10508	20315	2.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3315	13236	23040	0.88	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#65572) Homo sapiens cDNA clone GEN-037E11 5'
4573	10083	19900	13.92	7.5E-01	8922872	NT	Homo sapiens hypothetical protein FLJ10793 (FLJ10793), mRNA
9381	19042		3.57	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
9828	19329	25209	1.87	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885
9884	19368	25190	1.42	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1114	11029	20869	1.23	7.4E-01	AI698146.1	EST_HUMAN	trn14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2295	12177	22076	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3665	13579	23366	1.22	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4213	14111	23889	4.43	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7258	17135	27328	7.23	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9041	18828		3.28	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
9150	18901		1.59	7.4E-01	AI472841.1	EST_HUMAN	tr13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4515	14408	24194	0.95	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4602	14490	24277	4.76	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5127	14994		1.1	7.3E-01	5360211	NT	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5984	15889	26010	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
5984	15889	26011	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene

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6454	16315	26480	7.42	7.3E-01	M26511.1	NT	V.algindylifucus sucrose (scrB) gene, complete cds
6454	16315	26481	7.42	7.3E-01	M26511.1	NT	V.algindylifucus sucrose (scrB) gene, complete cds
8729	18355	28870	3.29	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
8729	18355	28871	3.29	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
814	10742		2.54	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (elf-2a) mRNA, complete cds
1914	11809	21687	3.68	7.2E-01	X79140.1	NT	N.tabacum Nelf-4A13 mRNA
2412	12289	22186	1.46	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3028	12956	22748	1.16	7.2E-01	AF198100.1	NT	Fowlbox virus, complete genome
3406	13323	23124	2.14	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3795	13707	23494	1.31	7.2E-01	BF339350.1	EST_HUMAN	602035589F1 NCI_OGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183222 5'
4680	14546	24335	2.41	7.2E-01	D90314.1	NT	L.resenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5064	14934	24706	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel α
5064	14934	24707	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel α
6923	16801	26994	1.21	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
7922	17772	28011	2.22	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276381 5'
8121	18009	28256	4.78	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
9570	19180		4.08	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
677	10610	20431	10.38	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3024	12952	22745	10.8	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4114	14014	23793	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4114	14014	23794	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
5623	15538	25625	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
5623	15538	25626	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6149	16022	26162	6.97	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
7669	17519	27746	2.25	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
9363	19550		1.61	7.1E-01	AA421492.1	EST_HUMAN	z106h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1209	11118	20966	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209	11118	20967	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	12277	22173	1.4	7.0E-01	N62412.1	EST_HUMAN	y273e07.s1 Soares_multiple_sclerosis_2Nbl-MSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2399	12277	22174	1.4	7.0E-01	N62412.1	EST_HUMAN	y273e07.s1 Soares_multiple_sclerosis_2Nbl-MSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4989	14864		1.95	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6880	16759		8.1	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8463	18336	28599	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
8463	18336	28600	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
954	10878	20725	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10878	20726	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1288	11196	21049	2.21	6.9E-01	AA593630.1	EST_HUMAN	nm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3399	13107	22911	1.63	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3399	13316	23117	0.85	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
6652	16532	26726	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6652	16532	26727	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8582	18450	28719	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8582	18450	28720	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
9016	19543		2.37	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
941	10866	20713	1.03	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2639	12506		1.16	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27127, 3418852-3573470
2799	11502	21362	1.58	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X86411.1ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4489	14363	24153	1.26	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
4749	14634	24420	0.83	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
7556	17407	27622	1.52	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
8437	18311	28566	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
8437	18311	28567	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
8458	18331	28593	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8458	18331	28594	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8619	18485	28757	1.79	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
295	10259	20080	29.34	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	10295	20110	19.53	6.7E-01	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA451864.1	EST_HUMAN	Zx12g12.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2120	12713	21908	3.59	6.7E-01	AF186073.1	NT	Drosophila melanogaster Msi85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2966	12893	22692	3.7	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4350	14246	24032	0.96	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	14762	24538	0.85	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCI_OGAP_Col17 Homo sapiens cDNA clone IMAGE:2574598 3'
5182	15046	24811	0.89	6.7E-01	AJ252942.1	NT	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial
5627	15542	25631	1.62	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
5817	15723	25836	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
5917	15723	25837	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6329	16192	26367	3.98	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
6342	16205	26367	1.46	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8323	18200	28449	2.23	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
8754	17903	28147	3.69	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2452	13329	22227	0.87	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2867	12532	22422	1.29	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13362	23168	1.04	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3608	13522	23310	3.05	6.6E-01	Y07669.1	NT	C. albicans random DNA marker, 282bp
4020	13924			6.5E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5822	15728	25840	3.96	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6525	16384	26563	3.63	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
7571	17422		2.41	6.6E-01	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9619	19197	25266	1.35	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
608	10544	20352	1.37	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	10544	20363	1.37	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3386	13304	23104	5.1	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
3951	13859	23633	1.08	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (L10RA) mRNA
4185	14085	23860	4.17	6.5E-01	AJ272285.1	NT	Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4215	14113	23890	0.86	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
4994	14869	24632	2.27	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5175	15041		0.88	6.5E-01	U37258.1	NT	Acetabacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellobiosyl diphosphopyrenol alpha-mannosyltransferase gene, complete cds
6036	15839	26071	1.38	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7919	17769	28008	2	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
8030	17922	28168	3.24	6.5E-01	H87583.1	EST_HUMAN	yr1706.r1 Soares_placenta_8to8weeks_ZN6HP8a9W: Homo sapiens cDNA clone IMAGE:252515 5'
8073	17964	28215	4.03	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
8170	18058		4.27	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone IMAGE:1007810 5'
8877	18689	28981	2.3	6.5E-01	AF014115.1	NT	Plasmidium berghelii cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
9419	19069		2.79	6.5E-01	BE465050.1	EST_HUMAN	h74ta10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
9651	19490		1.69	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
252	10218	20035	5.4	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3410	13327	23128	2.45	6.4E-01	U48954.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3785	13697	23484	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4389	14285	24066	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
4389	14285	24067	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
7007	16884	27076	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
7807	17657	27895	13.62	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
7818	17668	27908	1.44	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
9528	19135		6.34	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5'
9951	19553		1.65	6.4E-01	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
427	10372	20196	4.41	6.3E-01	P05228	SW/ISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
524	10466	20277	2.15	6.3E-01	U32589.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2116	12005	21903	3.87	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2534	12408	22300	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	12408	22301	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12911		0.93	6.3E-01	Y17275.1	NT	Lycopodium obscurum p69a gene, complete CDS

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3985	13892	23668	1.38	6.3E-01	X99675.1	NT	D.melanogaster mRNA for metabotropic glutamate receptor
6959	16837		3.17	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3969351 5'
7150	17027	27223	1.67	6.3E-01	S62927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
7421	17288	27495	2.72	6.3E-01	9627521	NT	Variola virus, complete genome
7421	17288	27496	2.72	6.3E-01	9627521	NT	Variola virus, complete genome
8004	17854	28095	1.4	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
8413	18288	28543	2.27	6.3E-01	AA877715.1	EST_HUMAN	m09h06.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK.
8647	18511	28791	11.72	6.3E-01	AI904160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
8725	18581	28865	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
8988	18690	28969	1.98	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
9128	19697	24899	9.21	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
9220	18944		1.54	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
9435	19619		1.58	6.3E-01	X83528.1	NT	C.limicola pscD gene
5578	15493	25569	2.12	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
6426	16287		3.06	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (CaSR-rs4) mRNA, partial cds
6831	16710	26903	5.45	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
7435	16448	26638	1.71	6.2E-01	BE362887.1	EST_HUMAN	601356146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
7476	17336		2.56	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
7799	17649	27886	7.14	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
8007	17857	28100	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2345	12225		4.5	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4931	14809	24577	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
4931	14809	24578	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
6104	15998	26134	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6104	15998	26135	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6792	16571	26863	3.72	6.1E-01	AF035353.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
7108	16985	27175	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7108	16985	27176	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7419	17286	27492	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
7419	17286	27493	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7778	17628	27860	1.59	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
486	10429	20243	0.92	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10490		2.64	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1339	11245	21103	1.76	6.0E-01	AF066253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3744	13656	23438	1.02	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5227	15151	24918	1.56	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5339	15280	25085	2.58	6.0E-01	AW139713.1	EST_HUMAN	U1-H-B11-aab-a-10-0-J1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
5940	15845	25968	2.61	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6350	16213	26375	6.2	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6725	16605	26794	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6725	16605	26795	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7653	17503	27727	1.69	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7894	17744		1.43	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
8411	18286	26541	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8411	18286	26542	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8838	18851	28939	2.74	6.0E-01	AI420623.1	EST_HUMAN	ff08f07 x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
9500	19115	25291	1.64	6.0E-01		NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
9787	19554	25065	2.1	6.0E-01	11421663 9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9809	19484		2.18	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
984	10907	20752	1.25	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	13156	22954	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3232	13156	22955	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4129	14029		4.12	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5889	15795	25917	2.1	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8061	17952	28203	2.67	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8328	18205	28454	3.1	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
8529	18401	28669	2.36	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
9165	18908	25342	1.91	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
9404	19057		2.18	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
9614	19193		4.15	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1867	11763	21637	1.44	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3902	13812	23596	0.96	5.8E-01	BF695738.1	EST_HUMAN	601652474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4413	14307	24090	2.81	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4990	14576		1.04	5.8E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Mgsxl) gene, partial cds, alternatively spliced products
5753	15861	25768	1.29	5.8E-01	ID78659.1	EST_HUMAN	HUM500E06B Human placenta poly(A) (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6077	16060		2.3	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6604	16484		2.62	5.8E-01	H41571.1	EST_HUMAN	yt91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
6764	16643	26830	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6764	16643	26831	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
7153	17030	27224	8.64	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8358	18235	28483	8.47	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8396	18272		3.23	5.8E-01	BF700082.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
8482	18355		1.78	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3186	13111	22915	1.48	5.7E-01	O9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3460	13376		2.43	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3929	13741	23533	1.65	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S7'2-BJ1S1) mRNA, partial cds
5201	15064	24827	2.24	5.7E-01	U78517.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
5936	15742	25854	3.72	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6100	15110	24874	1.41	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T-4 cDNA library under conditions of nitrogen deprivation
6564	16422	26603	2.12	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
9124	18883		1.68	5.7E-01	BE715051.1	EST_HUMAN	MR3-H10736-180700-003-a02 HT0736 Homo sapiens cDNA
3318	13239	23043	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	13239	23044	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3808	13720	23509	0.83	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4146	14046	23818	0.83	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
7111	16968	27180	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5'
7111	16988	27181	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5'
9023	18817		2.46	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
9137	18893	28794	1.73	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element ;
9524	19133		1.32	5.6E-01	P50805	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9919	19392		3.09	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1193	11103	20949	1.09	5.5E-01	89393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2668	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2668	12533	22424	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2888	12815	22608	1.34	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3027	12955		1.39	5.5E-01	J46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3196	13121	22926	3.1	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	13548	23335	1.29	5.5E-01	P48755	SWISSPROT	FOG-RELATED ANTIGEN-1
139	10113	19833	3.74	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	10113	19834	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	10509	20316	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
570	10509	20317	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
1260	11157	21006	2.24	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2059	11949		2.78	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2208	12095	21998	2.23	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
7738	17538	28557	2.01	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243690 5'
8427	18301	28557	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8892	18702	28996	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8892	18702	28997	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
9087	18862		2.12	5.4E-01	A1858398.1	EST_HUMAN	w137g04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
505	10447	20260	2.02	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2093	11982	21877	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	11982	21878	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2755	12617	22508	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	12617	22509	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3205	13129	22931	2.92	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (L-SL-C), gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4117	14017		1.29	5.3E-01	U3687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5350	15270	25098	1.75	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740711 5'
5350	15270	25099	1.75	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740711 5'
5467	15387	25447	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5467	15387	25448	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
7161	17038		2.15	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8846	18658	28946	5.62	5.3E-01	BE666291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
9015	19551		2.48	5.3E-01	AA916053.1	EST_HUMAN	0630e05.s1 NCI CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
799	10728	20568	11.31	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1148	11061	20904	7.69	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5(T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15)
1174	11096	20930	2.83	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1843	11739		5.04	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2099	11988	21886	2.75	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C095
3081	13008	22708	1.9	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3199	13124		1.22	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3359	13278		1.76	5.2E-01	AL116780.1	NT	Azotobacter vinelandii tcd gene for isocitrate dehydrogenase, complete cds
3397	13314	23114	1.9	5.2E-01	AA984165.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation am77g05.s1 Stratiagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3580	13494		1.13	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3582	13496	23287	1.06	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltractin (CAL T), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4949	14826		1.29	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
7761	17611	27837	1.28	5.2E-01	AF149352.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
9719	19280	25221	2.46	5.2E-01	AW137056.1	EST_HUMAN	U1-HB1-asp-a-08-0-J1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714798 3'
9887	19370		3.43	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR- DELTA)
601	10537	20347	1.89	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
632	10598	20381	3.28	5.1E-01	AJ233944.1	NT	Polygammum vitellinum (strain P1 vt1) 16S rRNA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
632	10589	20382	3.28	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1632	11536		1.06	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
1977	11870		1.44	5.1E-01	BF883095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
3984	13891	23667	3.84	5.1E-01	A1858495.1	EST_HUMAN	w39b12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4094	13994	23771	2.86	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6133	15980	26116	1.57	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
7584	17435	27650	4.54	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
7586	17437	27653	3.57	5.1E-01	W22302.1	EST_HUMAN	6651 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
9230	19478		3.62	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
9473	19100		2.03	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2087	11977	21871	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2087	11977	21872	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2097	11986	21882	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2097	11986	21883	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3698	13601	23388	0.84	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3797	13709	23495	3.44	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6951	16839		5.62	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
7442	16455	26644	3.61	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
7550	17401	27614	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)
7550	17401	27615	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)
7941	17791		1.27	5.0E-01	BE669218.1	EST_HUMAN	601445024F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3949436 5'
9003	18806	29099	9.32	5.0E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
9170	18913		2.26	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
9858	19349		2.02	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9869	19358		2.94	5.0E-01	Q13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.98	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1804	11760	21634	1.39	4.9E-01	U40809.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5679	15588	25688	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15588	25689	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6403	16267	26429	1.76	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
7359	19708		2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13n1), mRNA
9065	18346		1.43	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9851	19733		3.55	4.9E-01	AA613562.1	EST_HUMAN	in22e11.s1 NCL CGAP_Col10 Homo sapiens cDNA clone IMAGE:1144652 3'
4577	14136		1.12	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5381	15300	25153	8.94	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6018	15922		3.94	4.8E-01	AA659878.1	EST_HUMAN	nu85709.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
6330	16193		1.96	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D6S22298E) mRNA
6563	16421	26601	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26602	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6613	16493	26679	1.16	4.8E-01	AI820744.1	EST_HUMAN	yj77f10.y5 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element:
8111	18001		2.04	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
9369	19511		2.52	4.8E-01	AF227565.1	NT	Typanosoma cruzi transposon VIP II SIRE repeat region
9870	19359		2.26	4.8E-01	BE790632.1	EST_HUMAN	601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938909 5'
5925	15330	25953	8.36	4.7E-01	BF217173.1	EST_HUMAN	60183880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
8221	18103		5.77	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
8434	18308	26564	2.06	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
8692	18570	28853	2.43	4.7E-01	AW899448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
9390	19049		1.36	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2903198 3'
3674	13538	23375	1.27	4.6E-01	AW818633.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA
3683	13597	23383	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	13597	23384	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		0.97	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5360	15280	25111	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15280	25112	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78	4.6E-01	BE734781.1	EST_HUMAN	601569755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5414	15334	25384	3.29	4.6E-01	A1247679.1	EST_HUMAN	qt59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1;
5414	15334	25385	3.29	4.6E-01	A1247679.1	EST_HUMAN	qt59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.1;
5418	15339	25393	1.58	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6057	16040	26181	1.47	4.6E-01	U62332.1	NT	Emicella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057	16040	26182	1.47	4.6E-01	U62332.1	NT	Emicella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6843	16722	26916	13.48	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7363	17230	27430	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7363	17230	27431	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730	17580	27802	1.33	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7730	17580	27803	1.33	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
8359	18236	28495	2.86	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
8368	18245	28496	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8368	18245	28496	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8766	17915	28160	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8766	17915	28161	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
9313	19005		1.43	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
9978	19491		2.21	4.6E-01	AF120134.1	NT	Linanthus jamaicensis maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
1869	11765	21639	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1869	11765	21640	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2841	12759	22558	4.87	4.5E-01	AA677086.1	EST_HUMAN	z55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3275	13196	22996	3.97	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3331	13251	23056	1.05	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
3942	13850		1.41	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3982	13899	23665	1.1	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(IV) CHAIN
4085	15079		4.02	4.5E-01	AW873495.1	EST_HUMAN	ass96e09.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
							h660g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	BE9634445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406	15325	25375	1.45	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 P T0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	A1858849.1	EST_HUMAN	w32-02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
6897	16776	26970	3.14	4.5E-01	A1648596.1	EST_HUMAN	SWISNF COMPLEX 170 KDA SUBUNIT..
7100	16977		1.54	4.5E-01	11444786	NT	t55g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
7991	17841	28082	25.09	4.5E-01	M86006.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7991	17841	28083	25.09	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBCY17
9036	19724		2.25	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
9694	19245		1.44	4.5E-01	BF337531.1	EST_HUMAN	602036275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
9763	19283		2.15	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
9974	19652	24987	1.83	4.5E-01	AF238234.2	NT	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	6690503	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2340	12220	22118	3.59	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	13195	22994	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3274	13195	22995	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198	22998	1.87	4.4E-01	BF056726.1	EST_HUMAN	791d02.y1 NCI_CGAP_Brn16 Homo sapiens cDNA clone IMAGE:3383795 5'
4141	14041		1.33	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809393 5'
4924	14803		0.93	4.4E-01	BE141396.1	EST_HUMAN	MR0-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5326	15246	25050	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	15246	25051	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5490	15403	25474	1.3	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5499	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
5624	15539	25627	1.6	4.4E-01	A1198413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
5624	15539	25628	1.6	4.4E-01	A1198413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
5782	15688	25798	1.79	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2885510 3' similar to TR:Q95154 Q95154
6582	16462		10.84	4.4E-01	Z11679.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE.; S.tuberosum mRNA for induced stolon tip protein (partial)

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422	1.29	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
7723	17573	27798	1.99	4.4E-01	AI286650.1	EST_HUMAN	q639f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
7724	17574		2.45	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7813	17683	27903	4.67	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
7935	17785	28025	1.33	4.4E-01	S76404.1	NT	beta-HKA=HJK-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
7935	17785	28028	1.33	4.4E-01	S76404.1	NT	beta-HKA=HJK-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
9296	18986	28329	2.29	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
9306	19663		3.29	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9731	19267	28224	5.34	4.4E-01	9627742	NT	Autographa californica nucleopolyhedrovirus, complete genome
9824	19326		1.75	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
405	10351	20178	1.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
405	10351	20179	1.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1585	11489	21350	1.1	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2843	12771		0.95	4.3E-01	AW935299.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	12980	22742	0.93	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	13145		1.53	4.3E-01	AE000698.1	NT	Aquifex aeolicus section 30 of 109 of the complete genome
4059	13981	23737	1.15	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4306	10351	20178	1.02	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4306	10351	20179	1.02	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4875	14755		1.11	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5059	14929		1.06	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5600	15514	25592	3.04	4.3E-01	AF179825.1	NT	Salmix scitireus olfactory receptor (SSC186) gene, partial cds
6029	15933	26064	3.89	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica IfnG gene
6102	15986		4.01	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
6393	16255		2.54	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158296 5'
6909	16787		2.83	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
7608	17459	27674	1.85	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
7608	17459	27675	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
7872	17722	27967	1.27	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
8302	16049	26195	2.64	4.3E-01	AF075629.1	NT	TR-O00189 O00189 MJ-ADAPTIN-RELATED PROTEIN 2. ;
8537	18409	28673	1.98	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
8537	18409	28674	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
8537	18409	28674	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
9916	19390		2.02	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	12691	21089	1.04	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11800		0.89	4.2E-01	AA761653.1	EST_HUMAN	nt24409.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3558	13472	23263	4.78	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3585	13499	23288	1.09	4.2E-01	AI280338.1	EST_HUMAN	q1d407.1.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879045 3'
3803	13715	23503	0.96	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
3900	13810	23595	1	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4545	14438		3.63	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4599	14487	24273	4.96	4.2E-01	AA534093.1	EST_HUMAN	nt59h01.s1 NCI CGAP_P110 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25484	1.5	4.2E-01	BF242055.1	EST_HUMAN	60-1879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5533	15450	25518	1.56	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6151	16024	26165	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6184	19461	26219	2.1	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rats, W/F, spleen, Genomic, 419 nt, segment 2 of 2]
6217	16033	26233	5.91	4.2E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6663	16543	26739	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6663	16543	26740	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6776	16555	26844	1.19	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7992	17842	28084	1.48	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
8400	18276	28528	2.2	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
8699	18517	28789	2.04	4.2E-01	BE969485.2	EST_HUMAN	60-7660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
9863	19353		1.66	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF1 Homo sapiens cDNA clone HTF1H05 5'
1078	10994	20835	1.88	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1087	11003	20844	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1087	11003	20845	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1592	11496	21356	1.03	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2678	12543	22434	1.52	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	12836	22633	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12836	22634	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	13186	22985	1.13	4.1E-01	AA906344.1	EST_HUMAN	q194b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	14077	23552	2.59	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoC, isoD, isoE, isoF genes
4208	14107		1.07	4.1E-01	AA909257.1	EST_HUMAN	om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4373	14289		0.83	4.1E-01	R41726.1	EST_HUMAN	y911b03.st Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31814.3'
4567	14459	24247	1.26	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPOBDF10 5'
5185	15049		0.87	4.1E-01	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
5644	15557	25650	4.13	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6395	16257	26418	2.91	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
6683	16583	28757	1.3	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
7253	17130	27323	1.23	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
7888	17738		1.3	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
8018	17888		1.58	4.1E-01	BF349382.1	EST_HUMAN	GM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
8213	18097	28349	164	4.1E-01	X59700.1	NT	Zea mays ZMPM52 gene for 19 kDa zein protein
8698	17880	28121	2.79	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
9624	19702		1.72	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1023	10940	20783	1.27	4.0E-01	8404658	NT	Leaqueus rubellus mitochondrion, complete genome
1316	11223	21079	0.96	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1469	11374		4.06	4.0E-01	6879258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1960	12709	21742	1.17	4.0E-01	Z96933.1	NT	Ascolobolus immersus masc2 gene
1960	12709	21743	1.17	4.0E-01	Z96933.1	NT	Ascolobolus immersus masc2 gene
2774	10110	19931	1.09	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 componen n-recogin (Ubr1), mRNA
2939	12896	22665	2.24	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2939	12886	22666	2.24	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3637	13551	23339	1.61	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3755	13688	23451	3.24	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3755	13698	23452	3.24	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4712	14598		7.34	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5603	15517	25596	1.31	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
8959	18766		3.24	4.0E-01	L76030.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
9312	19597		2.22	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9825	19327		1.33	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
9910	19337		1.4	4.0E-01	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
227	10196	20007	1.59	3.9E-01	AW362188.1	EST_HUMAN	CV4-HT0136-150999-014-f09 HT0136 Homo sapiens cDNA
1356	11262	21119	2.1	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2605	12473	22367	3.54	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2673	12538	22427	5.98	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2673	12538	22428	5.98	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3058	12935	22776	3.63	3.9E-01	AJ225596.1	NT	Shorhizobium meliloti egl, syrB2, cys3 genes and orf3
3988	13395	23672	1.47	3.9E-01	BF592611.1	EST_HUMAN	7181d01.x1 NCI CGAP B16 Homo sapiens cDNA clone IMAGE:3339169 3'
4919	14798	24572	1.48	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC: 20 Homo sapiens cDNA clone IMAGE:3333699 5'
5613	15528	25611	3.53	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC: 53 Homo sapiens cDNA clone IMAGE:4082055 5'
7324	17200	27400	1.5	3.9E-01	AW195888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821
7503	17372	27581	1.4	3.9E-01	AI937337.1	EST_HUMAN	O94821 KIAA0713 PROTEIN ; wp76a02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5 HUMAN P48382 BINDING REGULATORY FACTOR. ;
7680	17530	27755	2.97	3.9E-01	M19879.1	NT	Human cladinin 27 gene, exons 10 and 11, and L1 and Alu repeats
8195	18080		2.22	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
9091	19642		2.49	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9209	18940		2.38	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
9288	18900	25328	1.26	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
154	10128		7.44	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1827	11724		1.22	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2524	12398	22289	2.44	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2591	12726	22362	4.41	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2972	12399		0.92	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3010	12938	22732	2	3.8E-01	AF043383.1	NT	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
3498	13355	23160	7.77	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3494	13410		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3506	13410		0.91	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3841	13752	23545	0.85	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2), mRNA
5045	14918	24692	0.98	3.8E-01	BE544953.1	EST_HUMAN	601074110F1 NIH_MGC: 12 Homo sapiens cDNA clone IMAGE:3460154 5'
5445	15396	25422	1.62	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
5994	15899	26023	4.47	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6053	16036	26177	3.81	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6498	16299		4.83	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
6980	16857	27052	3.07	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds

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7516	17304		4.11	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element contains PTTG repetitive element ;
8820	18633		2.82	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8939	18747	28041	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
8939	18747	29042	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
9297	18997		2.38	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
9422	19661		1.34	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
9530	19137		2.21	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
9917	19538		1.84	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
9921	19675	24993	1.37	3.8E-01	T54787.1	EST_HUMAN	y642b11.s1 Stragelene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
9937	19406	25180	1.3	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
9970	19430	25151	1.33	3.8E-01	AA776820.1	EST_HUMAN	ah37b01.s1 Soares testis_NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO DISTINCTIVE PROTEIN MOTIFS ;
2431	12308	22203	9.85	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3414	13331	23133	9.48	3.7E-01	AF056636.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4136	14036	23812	6.63	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4225	14123	23898	1.53	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4292	14190	23974	3.32	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6235	16101	26250	2.73	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6392	16254	26415	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6392	16254	26416	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6848	16727	26921	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
6848	16727	26922	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7307	17183		1.46	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
7894	17714	27958	3.93	3.7E-01	AI336411.1	EST_HUMAN	q146b07.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
8232	18113	28365	1.81	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
8392	18268	28518	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8392	18268	28519	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8762	17911	28155	4.23	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
8979	18784		2.76	3.7E-01	6977678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
9008	19303		1.87	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
9176	18917		1.94	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii psbA1 gene for outer membrane protein 1
9272	18976		2.41	3.7E-01	D88976.1	NT	Human mRNA for KIAA0223 gene, partial cds

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9634	19206		2.18	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9701	19251	25217	1.52	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9984	19746		1.31	3.7E-01	AJ237934.1	NT	Bos taurus partial stat5B gene, exons 2-15 and joined CDS
979	10902		7.17	3.6E-01	U89241.1	NT	Human mibp gene, partial cds
1292	11199	21054	2.59	3.6E-01	T80255.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1292	11199	21055	2.59	3.6E-01	T80255.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1874	11770	21645	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	11770	21646	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	11803	21682	6.18	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.03	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgr1 gene
2223	12108		1.04	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-01-1-g07 ST0171 Homo sapiens cDNA
2589	12460	22350	2.28	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2699	15077		8.9	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (euf3) mRNA, complete cds
3424	13341	23145	1.85	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4308	14206	23988	1.16	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4635	14523	24312	0.85	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4684	14570	24367	1.23	3.6E-01	AJ229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819	24587	2.01	3.6E-01	AW339393.1	EST_HUMAN	hg02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5899	15805	25928	1.6	3.6E-01	Y10196.1	NT	Homo sapiens PHFEX gene
6238	16104		5.49	3.6E-01	R94090.1	EST_HUMAN	y74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
6317	16180	26340	1.66	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares, thymus, NHFTh Homo sapiens cDNA clone IMAGE:2613010 3' similar to TR:O16117
6816	16696	26886	13.42	3.6E-01	AL161583.2	NT	O15117 FYN BINDING PROTEIN. [1]; Atabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17082	27269	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27270	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7674	17524	27750	15.34	3.6E-01	Q63194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS

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8314	18191	28440	1.94	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959997 5'
8453	18326	28585	3.69	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
8741	17890	28134	3.56	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
9044	19761		1.81	3.6E-01	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
9127	18886		3.05	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
9281	18983		3.03	3.6E-01	U68888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704		1.58	3.6E-01	AW190229.1	EST_HUMAN	x160e11.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN).
202	10174	16990	2.18	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
662	10596	20414	0.97	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
708	10640	20466	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10640	20467	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
763	10694	20531	3.17	3.5E-01	BF129786.1	EST_HUMAN	601811030R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1603	11508	21370	1.17	3.5E-01	BF310688.1	EST_HUMAN	601894633F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2563	12725	22327	1.85	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2672	12537		0.86	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	14065	23839	1.92	3.5E-01	AF071253.1	NT	Danio rerio hornedbox protein (hoxb5b) gene, complete cds
4379	14275	24056	1.29	3.5E-01	BE146885.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4790	14675	24462	0.84	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4849	14730	24513	3.84	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
6199	15959		3.47	3.5E-01	X98605.1	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
6704	16584		1.88	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
7612	17463	27680	1.51	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
7688	17538	27764	5	3.5E-01	Z26825.1	NT	X. laevis gene for albumin including HP1 enhancer
8116	18005	28251	2.99	3.5E-01	X61084.1	NT	C. griseus rhodopsin gene for opsin protein
8386	18263	28513	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8386	18263	28514	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8951	18758	29052	3.34	3.5E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	18937		2.12	3.5E-01	X64565.1	NT	B. taurus atpA1 gene for F0(F1) ATP synthase alpha-subunit
9941	19816	24999	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
9941	19816	25000	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	10624		1.9	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
960	10883	20731	4.53	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, of222 and partial inaA gene
1304	11211	21066	1.73	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2352	12232	22129	2.81	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2642	12509	22400	1.46	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12898	22697	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	12898	22698	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22846	5.41	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNCG1) mRNA, complete cds
3488	13404	23209	3.48	3.4E-01	AF106835.1	NT	Methyovirus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3722	13634		2.33	3.4E-01	BF449010.1	EST_HUMAN	7n84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
3965	13872		1.16	3.4E-01	AA584196.1	EST_HUMAN	Q9UJ15 DJ18C9.1 ;
4394	14290	24074	0.78	3.4E-01	AF166341.1	NT	no11b101 s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100347 3'
4544	14437	24221	1.82	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4628	14710	24494	0.93	3.4E-01	BE463761.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4870	14750		3.57	3.4E-01	AJ240973.1	EST_HUMAN	hy17409.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.13 L1 repetitive element ;
4970	14845	24614	1.2	3.4E-01	X16544.1	NT	qj95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5487	15406	25469	2.85	3.4E-01	AL161594.2	NT	Sea urchin hsp70 gene II for heat shock protein 70
5551	15467		4.71	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5654	15566		2.06	3.4E-01	L02971.1	NT	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
5715	15623	25724	2.57	3.4E-01	AW204505.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5780	15687	25786	1.47	3.4E-01	AL120544.1	EST_HUMAN	U1-HB11-ae1-e-12-Q-ULs1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6045	15948		1.52	3.4E-01	N95225.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
						EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:307342 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	18021	26161	1.41	3.4E-01	AI468082.1	EST_HUMAN	hm3g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
6943	16821		1.77	3.4E-01	AA337063.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7139	17016	27209	1.62	3.4E-01	9633624	NT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
7313	17189	27390	3.88	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
7313	17189	27391	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26635	4.17	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26636	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7690	17540	27766	2.22	3.4E-01	AJ225084.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
8380	18257		4.09	3.4E-01	AE000881.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8407	18233	28536	2.2	3.4E-01	P08925	SWISSPROT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
8440	18314	28572	2.26	3.4E-01	AF045981.1	NT	PROBABLE E4 PROTEIN
8604	18471	28742	1.77	3.4E-01	M25856.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28743	1.77	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8790	18605	28895	1.8	3.4E-01	AB035507.1	NT	Human von Willebrand factor gene, exons 36 and 37
8814	18627	28916	4.03	3.4E-01	AL161615.2	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
9020	18814		2.01	3.4E-01	U93604.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9130	18887		1.3	3.4E-01	Z21621.1	NT	Citrus variegation virus putative replicase gene, partial cds
9229	19508		1.82	3.4E-01	AF254351.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
9347	19024		4.9	3.4E-01	L26339.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
9378	19538		2.49	3.4E-01	BE218652.1	EST_HUMAN	Human autoantigen mRNA, complete cds
9432	19639		2.13	3.4E-01	9638361	NT	hva2h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
9537	19140	25264	1.79	3.4E-01	AJ297131.1	NT	PTR5 repetitive element ;
9829	19330		1.79	3.4E-01	AF019413.1	NT	Beta vulgaris mitochondrion, complete genome
14	10000	19791	7.91	3.3E-01	X07990.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
100	10000	19791	3.92	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
440	10384	20208	1.16	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
617	10554	20366	1.41	3.3E-01	7662485	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
1182	11093	20940	3.05	3.3E-01	Q12446	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
							Homo sapiens KIAA1100 protein (KIAA1100), mRNA
							PROLINE-RICH PROTEIN LAS17

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21046	4.82	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1588	11492	21352	1.11	3.3E-01	6753685	NT	<i>Mus musculus disintegrin 5 (Dign5)</i> , mRNA
1704	11605		1.05	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
2919	12846	22648	2	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeC3-12 complete genome
2982	12910		1.12	3.3E-01			INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3016	12944	22737	1.01	3.3E-01	O02743	SWISSPROT	Streptomyces argillaceus nifhamycin biosynthetic genes
3450	13367	23173	1.14	3.3E-01	AJ007932.2	NT	Homo sapiens MTA1-L1 gene, complete cds
3738	13650	23433	2.17	3.3E-01	AB012922.1	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	13829	23609	1.92	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4589	14477		1.48	3.3E-01	A1539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp.X57522 ANTIGEN
5263	15185	24960	2.68	3.3E-01	X89819.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
5263	15185	24961	2.68	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25623	2.71	3.3E-01	BE619650.1	EST_HUMAN	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25624	2.71	3.3E-01	BE619650.1	EST_HUMAN	60'472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64	3.3E-01	A1628131.1	EST_HUMAN	60'472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26149	3.64	3.3E-01	A1628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6575	16433	26616	1.5	3.3E-01	N85146.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6981	16858	27053	19.46	3.3E-01	BF683954.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
7477	17337	27542	3.26	3.3E-01	N69866.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
7507	17295	27504	2.81	3.3E-01	BF376745.1	EST_HUMAN	zac7h01.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7739	17589		2.07	3.3E-01	L41044.1	NT	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
8104	17994	28242	2.71	3.3E-01	X63953.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
8104	17994	28243	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8389	18265		1.82	3.3E-01	BF628499.1	EST_HUMAN	D.mauritiana Adh gene
8561	18431	28700	12.76	3.3E-01	BE219351.1	EST_HUMAN	602070802F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
							hw519g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8652	18541	28825	3.94	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8956	18763		4.79	3.3E-01	AA806621.1	EST_HUMAN	cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
8972	10000	19791	1.88	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
9119	18881	28789	1.63	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
9817	19323		6.05	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27)
449	10393		1.98	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	10634		2.05	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1145	11059	20902	18.99	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	11168	21019	1.04	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1368	11274	21130	6.25	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	11638	21506	1.22	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1744	11645	21513	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGC resequences, MAGD Homo sapiens cDNA
1744	11645	21514	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGC resequences, MAGD Homo sapiens cDNA
1800	11698	21574	1.16	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T-4 cDNA library under conditions of nitrogen deprivation
2114	12003	21901	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2494	12368		2.9	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pknx1), mRNA
2677	12542	22433	1.55	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3556	13470		0.96	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
3868	13779		0.97	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4295	14193	23977	1.35	3.2E-01	M19818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4397	14293	24077	1.33	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4632	14520		5.86	3.2E-01	BF983617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4907	15081		1.18	3.2E-01	M32352.1	NT	Mouse renin (Ren-1 d) gene, complete cds
5133	15000	24771	0.98	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5223	15146	24913	2.82	3.2E-01	BE173964.1	EST_HUMAN	CMD-HT0569-060300-259-f10 HT0569 Homo sapiens cDNA
6752	16631	26819	1.42	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
6872	16751	26946	13.32	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6875	16754	26951	14.29	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6929	16807		1.35	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
6986	16863	27056	1.5	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of the complete chromosome 1
7247	17124		2.19	3.2E-01	M8511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
7910	17760		3.25	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8058	17949	28199	2.7	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HFBDD21
9152	19682		3.28	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
9669	19228		2.97	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9801	19313		1.58	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9855	19696	24898	1.57	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2636	12503	22397	3.73	3.1E-01	R18051.1	EST_HUMAN	yes0106.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2665	12655	22419	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2655	12655	22420	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	12786		1.01	3.1E-01	AW629036.1	EST_HUMAN	hi46103.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3136	13061		2.78	3.1E-01	AB020069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3632	13744	23536	1.15	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5073	14943	24717	0.99	3.1E-01	AA576308.1	EST_HUMAN	nm61h05.s1 NCI_CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072761 3'
5365	15285	25119	8.66	3.1E-01	AF17611.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5447	15368		45.03	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5627	15444	25510	1.94	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
5890	15796	25918	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6160	19498	24861	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7023	16900	27092	1.87	3.1E-01	R45318.1	EST_HUMAN	y94601.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
7791	17641	27874	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7791	17641	27875	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17682	27926	1.96	3.1E-01	AJ244001.1	EST_HUMAN	q161e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
8211	18095	28348	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
8823	18636	28920	1.99	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
9279	18982		1.63	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
9315	19007		1.64	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
9457	19099		2.45	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9806	19318		3.11	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel α -
66	12635	19866	1.58	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
254	10220	20037	11.12	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1204	11114	20960	1.89	3.0E-01	AW300400.1	EST_HUMAN	xs6308.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1491	11396	21256	6.26	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2089	11978	21873					
3175	13100		0.86	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3789	13701	23488	0.98	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
4412	14306	24089	1.34	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0282-261199-001-g01 ST0282 Homo sapiens cDNA
5283	15205	24981	1.91	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5379	15288	25147	5.34	3.0E-01	BE741629.1	EST_HUMAN	601594980F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5401	15320	25368	3.18	3.0E-01	BE683576.1	EST_HUMAN	RC3-BT0333-180700-11-1-a03 BT0333 Homo sapiens cDNA
6086	16031	26171	3.18	3.0E-01	BE683576.1	EST_HUMAN	RC3-BT0333-180700-11-1-a03 BT0333 Homo sapiens cDNA
6335	16188	26358	3.51	3.0E-01	BE683576.1	EST_HUMAN	RC3-BT0333-180700-11-1-a03 BT0333 Homo sapiens cDNA
6429	16290	26451	2.61	3.0E-01	U01247.1	NT	Mus musculus 129/sv Ciara cell 10 kd protein (mCC10) gene, complete cds
6625	16506	26693	2.57	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6877	16756		1.35	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
6937	16815	27007	1.25	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7944	17794	28034			AE001755.1	NT	Thermotoga maritima section 67 of 138 of the complete genome
8980	18785	29074	4.67	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f9), mRNA
8980	18785	29075	1.27	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881594 5'
9564	19647		1.89	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpaA gene for ER chaperone BIP, complete cds
9836	19690		2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
1978	11871	21762	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
2201	12088	21989	1.43	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
3147	13072	22873	2.76	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rplia), mRNA
3213	13137	22939	1.6	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3213	13137	22940	0.99	2.9E-01	AF222718.1	NT	Chrysididymus synuroideus mitochondrion, complete genome
			1.03	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
			2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
			2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3821	13733	23522	1.28	2.9E-01	AI010830.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2189412.3' similar to gp:D15050 NIL-2-A
3994	13901		0.82	2.9E-01	AW002902.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4384	14280	24059	1.01	2.9E-01	AA284468.1	EST_HUMAN	w02f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395.3'
4388	14284	24064	0.78	2.9E-01	AF134119.1	NT	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591.5' similar to contains Alu repetitive element;
4388	14284	24065	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	14615	24401	0.92	2.9E-01	AB019029.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
5218	15141		1.49	2.9E-01	R37485.1	EST_HUMAN	Mus musculus gene, complete cds, similar to EXLM1
5522	15440	25504	4.45	2.9E-01	X56098.1	NT	y77e12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291.3'
5522	15440	25505	4.45	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5529	15448	25513	5.83	2.9E-01	6879662	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5818	15724	25838	2.24	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6171	15128	24847	1.51	2.9E-01	AF142329.1	NT	Bos taurus myosin I mRNA, complete cds
6218	16084	26234	2.52	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Lgih protein (Lgih) gene, partial cds
6249	16115	26267	1.74	2.9E-01	AF100956.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR508C
6619	16499	26686	1.76	2.9E-01	BE540422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
6619	16499	26687	1.76	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287.5'
8267	18147	28387	1.96	2.9E-01	AF128843.1	NT	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287.5'
8502	18375	28639	2.69	2.9E-01	V01394.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
8502	18375	28640	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8864	18676	28965	1.77	2.9E-01	AA935373.1	EST_HUMAN	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8866	18678	28967	4.54	2.9E-01	AL139078.2	NT	ny35h02.s1 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.t2 LTR8 repetitive element;
9514	19127	25260	1.53	2.9E-01	AW005671.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
9602	19184	25248	2.74	2.9E-01	AF092453.1	NT	wz88f05.x1 NCI_CGAP_Bm25.Homo sapiens cDNA clone IMAGE:2565921.3' similar to contains element MER29 repetitive element;
9644	19212		1.33	2.9E-01	BE788199.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
9883	19367	25188	4.86	2.9E-01	Y08937.1	NT	601482059F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884559.5'
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
556	10497		1.84	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1067	10983	20828	2.47	2.8E-01	AF168050.1	NT	Guirra guirra oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11163	21013	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1256	11163	21014	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1269	11176	21025	1.01	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1696	11598	21470	1.55	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0384-120200-065-b05 CT0384 Homo sapiens cDNA
1966	11860	21750	1.77	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2084	11974	21869	1.47	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2423	12300	22197	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2630	12498	22388	1.37	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2940	12867		1.49	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90KDa heat-shock protein (HSP90) mRNA, partial cds
2941	12868	22667	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	12868	22668	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3332	13252	23057	1.1	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (417)
3915	13824	23604	1.75	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	14003		2.21	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4352	14248	24034	0.98	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Mega9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038	2.2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14559	24352	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14559	24353	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14608	24394	2.8	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4755	14640	24427	1.54	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4787	14672	24459	1.7	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5252	19440	24948	21.36	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5443	15363	25419	2.33	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	15677	25764	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
5770	15677	25785	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6038	15941	26073	7.67	2.8E-01	BF511215.1	EST_HUMAN	UHH-B14-aci-f04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3065182 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16593	26781	1.24	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN)
6713	16593	26782	1.24	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN)
6778	16657	26847	2.39	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6894	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
7311	17187	27388	1.35	2.8E-01	AF080592.1	NT	Mus musculus centrin (Cetn2) gene, complete cds
7600	17451		1.15	2.8E-01	L13654.1	NT	Lycopodium esculentum peroxidase (TPX1) mRNA, complete cds
7789	17639	27872	2.79	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
8126	18014	28261	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8126	18014	28262	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8153	18041	28291	3.01	2.8E-01	BF695970.1	EST_HUMAN	601882148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
8254	18134	28382	2.62	2.8E-01	AF051662.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8599	18486		3.49	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
9552	19150		6.37	2.8E-01	DB3329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
9657	19219	25236	3.11	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
9826	19651		1.69	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
597	10533	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	zx39b10.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1240	11147	20996	1.49	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1604	11509		1.73	2.7E-01	X79815.1	NT	G. lamblia SR2 gene
1698	11600	21471	2.96	2.7E-01	W58067.1	EST_HUMAN	z422h10.r1 Soares, fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1738	11639	21507	1.25	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P'15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2088	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2316	12197	22094	8.78	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial repetitive element;
2406	12283	22180	3.51	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046536 3' similar to contains element L1
2956	12863		1.25	2.7E-01	BF066284.1	EST_HUMAN	GM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3929	13838	23618	1.88	2.7E-01	A1928015.1	EST_HUMAN	w092e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3943	13851	23626	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4796	14681	24468	0.89	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds

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4973	14848		3.5	2.7E-01	AW856131.1	EST_HUMAN	RC1-C10286-230200-0'16-e03 C10286 Homo sapiens cDNA
5221	15144	24838	3.49	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
6064	16047	26192	2.25	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6527	16386	26565	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7378	17247	27453	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7378	17247	27454	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7379	17248		2.24	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
7801	17651	27888	1.29	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
7827	17677	27921	1.93	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
8187	18073	28322	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8187	18073	28323	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8197	18082	28333	4.09	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9366	19034		1.27	2.7E-01	X95287.1	NT	G.gallus mRNA for ryanodine receptor type 3
9810	19320		2.15	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
462	12667	20224	1.54	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	10416		1.39	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1371	11277	21133	2.23	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1418	11324	21188	0.97	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	11750	21624	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	11750	21625	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04410.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S
2046	11937		9.9	2.6E-01	AW733152.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2106	11995	21895	1.2	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2424	12301		2.68	2.6E-01	Y12936.1	NT	B. maritimus tbcL gene
2499	12374		9.68	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690043 5'
3053	12990		1.03	2.6E-01	AW974531.1	EST_HUMAN	EST386635 IMAGE reserences, MAGM Homo sapiens cDNA
							h30c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.13 L1 repetitive element;
3485	13401		0.94	2.6E-01	BE217816.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3532	13448	23245	1.12	2.6E-01	M22342.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3591	13505	23295	1.7	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23351	0.9	2.6E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23691	1	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4062	13964	23742	13.13	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4259	14158	23935	0.95	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457617.1	EST_HUMAN	aa89407.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4548	14441	24224	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4616	14504	24292	1.28	2.6E-01	AF142703.1	NT	Ophrestia radicata matura-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4896	14776	24554	3.66	2.6E-01	H04858.1	EST_HUMAN	yj5'e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	14923	24696	0.86	2.6E-01	P08503	SWISSPROT	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5700	19764		2.03	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
5763	15670	25777	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
5763	15670	25778	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6552	16410	26588	1.52	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517.U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6585	16465	26656	1.27	2.6E-01	R02411.1	EST_HUMAN	ys82a07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124212 5'
6852	16731	26925	3.01	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150396 5'
6900	16779	26973	2.04	2.6E-01	Q10199	SWISSPROT	HYPOPHOSPHATASE 2 KD PROTEIN C11C11.02 IN CHROMOSOME II
7046	16923	27112	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-E T0082-310500-021-F10 ET0082 Homo sapiens cDNA
7046	16923	27113	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-E T0082-310500-021-F10 ET0082 Homo sapiens cDNA
7654	17704		1.16	2.6E-01	Q28296	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18625		93.65	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9136	18892		1.98	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
9328	19655		1.92	2.6E-01	BE883491.1	EST_HUMAN	601511032F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
9395	19053	25309	2.6	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9833	19333		6.03	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9899	19376		1.5	2.6E-01	Q07631	SWISSPROT	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE)
241	10209	20025	2.12	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025	1.86	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.5E-01	M26501.1	NT	Starfish (P ochraceus) cytoplasmic actin gene, complete cds
815	10743	20589	1.32	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1044	10982		1.86	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20864	9.5	2.5E-01	T98937.1	EST_HUMAN	ye11g07.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1503	11407	21266	0.85	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1697	11599		5.43	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612	0.88	2.5E-01	BE96604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1840	12706	21613	0.88	2.5E-01	BE96604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2357	12237		8.29	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2446	12323		1.35	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:584862 5'
2597	12466	22359	0.97	2.5E-01	X95310.1	NT	B. laurus mRNA for D-aspartate oxidase
3366	13285		2.87	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3490	13406	23211	0.86	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3502	13419	23220	7.93	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3774	13686	23468	1.15	2.5E-01	A1741483.1	EST_HUMAN	wg1c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3774	13686	23469	1.15	2.5E-01	A1741483.1	EST_HUMAN	wg1c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3977	13884		0.83	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120		1.2	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4514	14407	24193	0.96	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4643	14531		1.14	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4649	14535	24324	3.78	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4672	14558	24351	2.19	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4698	14584		3.16	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4726	14612	24398	0.79	2.5E-01	BE966785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4750	14535	24421	0.89	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR
5169	15035	24802	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5169	15035	24803	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5264	15186	24962	11.62	2.5E-01	S83330.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2630 nt]
6366	16229		1.32	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
6500	16359	26532	3.73	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6583	16463	26655	2.99	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares_N3F_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
6788	16667	26858	2.25	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862809 5'
7020	16997	27087	3.95	2.5E-01	H53236.1	EST_HUMAN	yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
7481	17351	27554	16.11	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7481	17351	27555	16.11	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7522	17341	27547	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7522	17341	27548	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7814	17664	27904	1.5	2.5E-01	AW681997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
8010	17860	28105	1.62	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_UK1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8011	17861	28106	1.68	2.5E-01	X68491.1	NT	Mouse L1Md LINE DNA
8426	18300	28556	2.32	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
9074	18551	29117	2.45	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
9100	19729		4.2	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9559	19581	28072	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
541	10482	20292	1.53	2.4E-01	AA936316.1	EST_HUMAN	on70404.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
830	10757	20608	2.38	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1282	11190	21041	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1282	11190	21042	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1362	11268	21123	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FLJ-1 gene, partial
1808	11705		24.08	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1858	11754	21629	1.41	2.4E-01	AF251708.1	NT	Zoocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	11960	21875	0.88	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2122	12010		1.16	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2215	12101	22005	2.01	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2491	12366	22260	1.63	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2734	12506	22491	2.14	2.4E-01	X71783.1	NT	D.discoideum (A3-K) porA gene
2756	12618	22510	6.63	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3093	13020						Bovine adenovirus 3 complete genome
3109	13035	22831	2.82	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
4817	14700	24486	0.88	2.4E-01	BE160080.1	EST_HUMAN	H.sapiens AGT gene, PstI fragment of intron 4
4981	14856	24622	50.15	2.4E-01	D00944.1	NT	QV1-HT0412-020400-130-b10 HT0412 Homo sapiens cDNA
5469	15389	25451	7.53	2.4E-01	AF091216.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5469	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5593	15508	25583	2.13	2.4E-01	BF592336.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
5642	15555	25648	2.66	2.4E-01	AF035546.1	NT	7f54d04.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5705	15613	25714	2.15	2.4E-01	7661801	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element ;
5937	15842	25966	1.79	2.4E-01	AI698989.1	EST_HUMAN	Drosophila melanogaster p38a MAP kinase gene, complete cds
6345	16208	26371	8.87	2.4E-01	L43001.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6860	16739	26931	1.62	2.4E-01	AJ012585.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
7517	17306	27511	6.72	2.4E-01	AI698515.1	EST_HUMAN	wc62c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7965	17815	28056	1.93	2.4E-01	Q03692	SWISSPROT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
8149	18037	28285	3.63	2.4E-01	AL161494.2	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8209	18093	28347	1.99	2.4E-01	AF030199.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8634	18406		2.42	2.4E-01	Z12647.1	NT	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
9030	18821	29109	1.55	2.4E-01	AF217491.1	NT	MER22.b1 TAR1 repetitive element ;
9162	19526		2.39	2.4E-01	AF004213.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
9222	18945		2.54	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
9439	19509		1.59	2.4E-01	V01507.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
9650	19716		1.26	2.4E-01	BF229975.1	EST_HUMAN	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9855	19355		3.35	2.4E-01	AL163281.2	NT	Gallus gallus gene coding for a-actin
383	10330	20153	0.9	2.3E-01	AF58898.1	NT	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081
							aromatase [P.oephila guttata=zebra finches, ovary, mRNA, 3188 nt]

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	10568		4.42	- 2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	10587	20403	19.84	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
918	10842	20687	3.35	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1494	11398	21258	1.5	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1546	11451		0.88	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1586	11490	21351	1.38	2.3E-01	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
1614	11518	21378	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	11892		1.3	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2396	12274	22160	1.56	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2615	12483	22372	1.02	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2794	11271	21127	0.88	2.3E-01	AB015033.1	NT	Marinibacteria agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2934	12861	22661	1.29	2.3E-01	AA601379.1	EST_HUMAN	no16d06.st NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element ;
3045	12972		5.73	2.3E-01	R21732.1	EST_HUMAN	yt21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3324	13244	23051	1.09	2.3E-01	H69836.1	EST_HUMAN	yr97h10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:273283 5'
3766	13679	23461	1.11	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	13767		3.72	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926	0.85	2.3E-01	R82252.1	EST_HUMAN	y17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4300	14198		3.35	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	14245	24031	1.02	2.3E-01	D90899.1	NT	Synechocystis sp. PC06803 complete genome, 1/27, 1-133859
4396	14282	24051	2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4956	14668	24455	0.82	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24641	0.95	2.3E-01	BF316135.1	EST_HUMAN	601886136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5101	14969	24745	0.98	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (h-LA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5146	15013	24783	26.95	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15189	24942	2.6	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074	1.71	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	15314	25361	4.83	2.3E-01	X95587.1	NT	C. familiaris rom1 gene
5618	15533	25617	1.87	2.3E-01	A1708840.1	EST_HUMAN	as27et12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5618	15533	25618	1.87	2.3E-01	A1708840.1	EST_HUMAN	as27et12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16005	26142	3.93	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
6384	16246	26408	2.62	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6487	16345	26519	3.19	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
6491	16349	26519	1.59	2.3E-01	BE888071.1	EST_HUMAN	60'511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
6560	16418		2.9	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
6664	16544	26741	2.28	2.3E-01	M69931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7657	17507	27732	1.37	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (-hincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
7712	17562	27787	2.54	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
7740	17590	27811	2.26	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
7974	17824		4.95	2.3E-01	BF133377.1	EST_HUMAN	60'646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
8525	18397	28663	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8525	18397	28664	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8658	18547	28830	2.39	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AF39, section 4 of 94 of the complete genome
9144	18898		2.53	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
9232	18951		20.46	2.3E-01	T27231.1	EST_HUMAN	HCOEST144 HT28M6 Homo sapiens cDNA clone HCOE44 5'
9268	19477		1.65	2.3E-01	AA089819.1	EST_HUMAN	chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9266	18970		2.07	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
9324	19665	24990	2.05	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element ;
9358	19708	24905	4.88	2.3E-01	BE882464.1	EST_HUMAN	60'507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908889 5'
9407	19060		1.93	2.3E-01	BF663319.1	EST_HUMAN	602144456F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
9456	19086		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19088		4.54	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9793	19310		2.67	2.3E-01	BF475611.1	EST_HUMAN	nacc39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10098	19885	0.96	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1545	11450	21311	3.13	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11865	-	0.91	2.2E-01	AF171901.1	NT	Timaresurus malabaricus cyb gene, partial cds: mitochondrial gene for mitochondrial product
2042	11933	21829	2.78	2.2E-01	M34640.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2354	12234	22131	6.24	2.2E-01	BF677538.1	EST_HUMAN	602086608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2543	12417	22307	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2543	12417	22308	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2853	12781	22570	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2853	12781	22571	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2890	12817	-	1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3346	13266	-	2.67	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	13655	-	1.05	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23688	0.81	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018	-	1.19	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
4166	14066	23840	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4166	14066	23841	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4258	14157	23833	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4258	14157	23934	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4399	14284	24078	1.09	2.2E-01	Z54148.1	NT	B. abortus bp26 gene
4719	14505	-	1.22	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	14610	24396	2.47	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4891	14771	24549	1.19	2.2E-01	M86524.1	NT	Human dystrophin gene
4975	14850	-	1.2	2.2E-01	L13298.1	NT	Mus musculus vinculin gene, exon 3
5513	15431	25495	1.71	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5518	15436	-	3.99	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6189	16074	26223	10.59	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6376	16556	-	2.19	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7217	17094		2.29	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
7304	17180	27382	1.39	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
7353	17221	27421	1.4	2.2E-01	W02988.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA IMAGE:291591 5'
7366	17344	27550	13.13	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522	3.98	2.2E-01	M89643.1	NT	Brachydanio rerio apendymin beta and gamma chains (Epd) gene, complete cds
							Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
7648	17498	27720	3.57	2.2E-01	AF197941.1	NT	nuclear gene for chloroplast product
7719	17509	27794	2.2	2.2E-01	BF206507.1	EST_HUMAN	601669724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8723	18540	28824	4.94	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
8756	17905	28149	2.91	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
9077	18854		2.2	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltratin (CAL T), NAD(P)H dehydrogenase-like protein (NSDHL), and Lp
9183	19720		3.72	2.2E-01	U82671.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
9269	18973		2.34	2.2E-01	AF188843.1	NT	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9379	15093	24887	2.56	2.2E-01	AW361098.1	EST_HUMAN	AV694801 GK Homo sapiens cDNA clone GKCAHB02 5'
9875	19713		3.75	2.2E-01	AV694801.1	EST_HUMAN	nm31e11.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
985	10879	20727	1.74	2.1E-01	AA569289.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
988	10881	20729	0.9	2.1E-01	AL161504.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1108	11023		2.16	2.1E-01	AE002314.2	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20935	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11767	21642	1.84	2.1E-01	AA906824.1	EST_HUMAN	ok73s02.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2111	12000	21899	3.08	2.1E-01	BF995073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
							602063129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2894	12821	22613	1.65	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3736	13548		5.05	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
3967	13874	23651	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
3967	13874	23652	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178		1.28	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4474	14368	24157	1.21	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4766	14651	24439	1.26	2.1E-01	AJ009784.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5134	15001	24772	0.99	2.1E-01	M98261.1	NT	Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds
5243	15167	24938	5.99	2.1E-01	BF672895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6123	15970	26106	1.86	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
6386	16247		1.97	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6535	16393	26572	1.74	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6559	16417	26596	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6559	16417	26597	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16585		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1B), mRNA
6951	16829	27022	4.78	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
7224	17101	27289	5.88	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
7479	17349	27553	2.36	2.1E-01	X97378.1	NT	A.thaliana mRNA for ATRAP1b protein
7547	17398	27611	1.19	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
7917	17767	28006	2.49	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
7929	17779	28018	1.49	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
8849	18661		2.31	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
8862	18674	28964	2.15	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
9522	19132		1.6	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
9730	19634		1.4	2.1E-01	L32588.1	NT	Human granulin gene
9905	19382	25174	1.29	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3223034 3'
9979	19436		1.29	2.1E-01	5835904	NT	Salvelinus alpinus mitochondrion, complete genome
193	10165	19983	1.72	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avana, complete cds
523	10465		2.39	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
684	10617	20440	1.19	2.0E-01	M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
793	10722	20563	1.81	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
995	10915	20759	1.03	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915
1109	11024	20866	2.57	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11141	20993	1.42	2.0E-01	AJ132895.5	NT	Homo sapiens rac1 gene
1286	11194	21047	1.29	2.0E-01	AW384937.1	EST_HUMAN	PM1-H10422-291299-002-c06 HT0422 Homo sapiens cDNA
1471	11376	21241	13.51	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	11442	21300	1.59	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1688	11590		1.82	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1723	11624		1.64	2.0E-01	U67525.1	NT	Malhanococcus jannaschii section 67 of 150 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC: 65 Homo sapiens cDNA clone IMAGE:3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC: 65 Homo sapiens cDNA clone IMAGE:3853330 5'
2299	12181		1.67	2.0E-01	X82877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene
2861	12789		0.95	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH85A11
3442	13359	23166	0.8	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3646	13560	23346	0.81	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
3945	13863	23628	0.8	2.0E-01	X83997.1	NT	C.parasitica eapC gene
4464	14358		8.47	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4859	14739	24519	1.07	2.0E-01	AF147083.1	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
4972	14847	24616	6.07	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5041	14913	24687	1.1	2.0E-01	Y19216.1	NT	Homo sapiens putative psithHbD pseudogene for hair keratin, exons 1 to 9
5342	15283	25089	2.55	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5570	15428	25491	2.73	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5694	15603	25705	5.29	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
5874	15780	25900	4.31	2.0E-01	X61033.1	NT	M. auratus mu class glutathione transferase gene
5934	15899	25962	3.54	2.0E-01	AW360895.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
6637	16517		6.95	2.0E-01	AF028028.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
6772	16651	26839	4.18	2.0E-01	X91151.1	NT	M. musculus scp2 gene exon 14
7511	17299		4.39	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7692	17542		2.07	2.0E-01	AF148692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17624	27857	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
7774	17624	27858	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28350	2.7	2.0E-01	D89086.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
8214	18098	28351	2.7	2.0E-01	D89086.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF208637.2	NT	Pirenephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9747	19308	28202	3.22	2.0E-01	A023582.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
9769	19288		6.61	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9897	19374	25193	1.5	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
105	10086		10.35	1.9E-01	7549743	NT	Rattus norvegicus Ary hydrocarbon receptor nuclear translocator 1 (Ahrnt), mRNA
349	10308	20128	6	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
640	10577	20392	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
640	10577	20393	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
647	10584	20400	5.37	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
648	10584	20400	7.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
970	10893		1.61	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1088	11004	20846	9.3	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1348	11254	21110	2.3	1.9E-01	AF081282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322		3.91	1.9E-01	AF184523.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2330	12211	22109	3.31	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2892	12819	22611	3.91	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2908	12834		5.55	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3349	13269	23072	3.4	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	13351	23156	4.63	1.9E-01	R16467.1	EST_HUMAN	VF42T10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129647 5'
3735	13647	23432	0.93	1.9E-01	AF294017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3762	13675	23457	0.96	1.9E-01	P39768	SW/ISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3910	13820	23600	3.02	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3992	13899	23676	1.89	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4138	14038	23813	1.06	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4369	14265	24049	0.89	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4662	14548	24338	0.84	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carboxyl phosphate synthetase III, myosin light chain, MAP2
4912	14791	24566	0.86	1.9E-01	AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
4943	14821		1.04	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
4962	14837	24605	1.11	1.9E-01	O95239	SW/ISSPROT	KINESIN-LIKE PROTEIN KIF4
5031	14903	24675	1.03	1.9E-01	AJ251176.1	NT	Phoca vitulina partial ar2B gene for alpha adrenergic receptor 2B
5113	14981	24755	0.99	1.9E-01	Z70296.1	NT	S.mansoni elastase HP1 gene
5123	14991		1.19	1.9E-01	A1631199.1	EST_HUMAN	ts93g12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:238886 3' similar to gb:M21574 ALPHA
5153	15020	24789	0.99	1.9E-01	5679095	NT	PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA
5441	15361		4.28	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5466	15386	25446	7.67	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5588	15503		2.26	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6162	15119	24863	1.7	1.9E-01	R43212.1	EST_HUMAN	yg09at12.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
6423	16284	26446	1.43	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB) gene, complete cds
6449	16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
6658	16538	26735	1.62	1.9E-01	AL161657.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8038	17930	28176	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8038	17930	28177	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8137	18025	28271	1.75	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8961	18768	29060	2.61	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9546	19146		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
9880	19546		1.26	1.9E-01	AF001188.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
29	10016	19811	2.26	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
260	12663	20041	1.22	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
366	10322	20145	2.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	10661	20493	2.15	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
966	10889	20735	0.85	1.8E-01	AI91212.1	EST_HUMAN	wd71f02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1075	10990	20832	1.21	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1267	11174	21024	5.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1487	11392	21262	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1487	11392	21253	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1803	11700		0.92	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	11720		1.93	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;
1873	11769	21644	1.5	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A9 precursor, complete cds
2660	12527		2.99	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081289-036-g04 DT0018 Homo sapiens cDNA
2868	12796		1.61	1.8E-01	AF184589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2873	12800	22595	1.09	1.8E-01	AW182300.1	EST_HUMAN	x141a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3085	13012	22803	1.28	1.8E-01	AW995176.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	13484	23275	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3570	13484	23276	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4154	14054	23828	0.8	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4238	14137		1.13	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4456	14350	24141	5.12	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663	14549	24339	2.36	1.8E-01	AB051897.1	NT	Mus musculus Soya6, Soya6, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4700	14586	24377	0.93	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4977	14852	24618	1.77	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5027	14900	24670	4.17	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	14925	24697	1.28	1.8E-01	AI439881.1	EST_HUMAN	tt57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134890 3'
5117	14985		1.03	1.8E-01	AJ000742.1	NT	Homo Sapiens histH1 gene, 5' UTR
5549	15465	25535	1.41	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5922	15827	25952	1.29	1.8E-01	Q9QY14	SW/ISSPROT	FORKHEAD BOX PROTEIN E3
5948	15853		2.5	1.8E-01	N94853.1	EST_HUMAN	y62h02.r1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6179	16065	26214	1.38	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
6179	16065	26215	1.38	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7382	17251	27456	1.72	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.8E-01		NT	Bacteriophage like, complete genome
7933	17783	28022	1.19	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
8033	17925	28172	3.19	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
8118	16065	26214	2.9	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
8118	16065	26215	2.9	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
8119	18007	28254	3.88	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG104) gene, complete cds
8381	18258	28507	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
8758	17907	28152	3.98	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
8976	18781	29073	2.83	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
9169	18912	25344	1.65	1.8E-01	BF346823.1	EST_HUMAN	602019928F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156318 5'
9625	19200		2.05	1.8E-01	Q96682	SW/ISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R24494.1	EST_HUMAN	yf48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9779	19294		1.63	1.8E-01	Y1114.1	NT	E. dispar mRNA for hexokinase (hpk1)
563	10503	20309	1.8	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
788	10717	20559	2.04	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
945	10870		1.89	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1042	10960	20802	1.6	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1042	10960	20803	1.6	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1938	11833		3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	12758	22548	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	12758						
2829	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2896	12823	22616	1.74	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2967	12894	22693	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
2967	12894	22694	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3067	12994	22785	1.89	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3401	13318	23119	1.96	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3557	13471	23262	1	1.7E-01	AJ24877.1	NT	Homo sapiens hapt1 gene, complete CDS
3559	13770	23562	4.41	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4459	14353		1.88	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4732	14617	24403	1.4	1.7E-01	AJ247635.1	EST_HUMAN	qf57e09.X1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848608 3' similar to contains ORF.b1 ORF repetitive element;
4986	14861		1.16	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5067	14937		1.18	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI CGAP Co8 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI CGAP Co8 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5820	15726	25839	12.31	1.7E-01	H72118.1	EST_HUMAN	y502g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6112	16006		2.15	1.7E-01	AF02652.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6320	16183	26344	7.96	1.7E-01	BE794179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6588	16468	26658	1.2	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
6814	16693	26882	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6814	16693	26883	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
7066	16943	27135	2.46	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
7531	17382	27693	7.38	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
7601	17452	27666	2.06	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7942	17792	28032	1.48	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	nc60e07.s1 NCI_CGAP_Oc9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
8067	17958	28208	9.13	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
8182	18068	28317	2.47	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
8456	18329	28589	7.88	1.7E-01	7106300	NT	ot43a03.s1 NCI_CGAP_GNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
8456	18329	28590	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8949	18757		1.92	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
9012	18811	29107	4.38	1.7E-01	11418157	NT	AMP NUCLEOSIDASE
9139	19666		1.5	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1L), mRNA
9420	19513		1.28	1.7E-01	A824404.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
9705	19253	25218	5.79	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
120	10097	19917	1.88	1.6E-01	AF217632.1	NT	Human beta globin region on chromosome 11
664	12641	20416	1.53	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1505	11409	21268	4.05	1.6E-01	AF298117.1	NT	yh75f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1882	11778	21653	2.4	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1941	11836		1	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2335	12719	22115	0.96	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2443	12320	22218	2.19	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2863	12791	22583	8.9	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22584	8.9	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23285	1.31	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23286	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3919	13828		2.61	1.6E-01	AE004413.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
							Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4234	14132	23908	7.92	1.6E-01	AF179380.1	NT	Homo sapiens apelin gene, complete cds
4353	14249		2.44	1.6E-01	AW968601.1	EST_HUMAN	EST380877 MAGE resequences, MAGJ Homo sapiens cDNA
4361	14257		4.01	1.6E-01	6763319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	14665	24451	0.86	1.6E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4781	14665	24452	0.86	1.6E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24524	1.14	1.6E-01	AA088343.1	EST_HUMAN	284409.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4869	14769	24546	1.92	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
4889	14769	24547	1.92	1.6E-01	AJ006356.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
4958	14833	24601	1.09	1.6E-01	BE018707.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5390	15309	25162	3.12	1.6E-01	AW197496.1	EST_HUMAN	b683h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5390	15309	25163	3.12	1.6E-01	AW197496.1	EST_HUMAN	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
5398	15317	25364	2.07	1.6E-01	AF034716.1	NT	xm43f01.x1 NCI_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5873	15779	25899	2.24	1.6E-01	AL161588.2	NT	HYPOTHETICAL 127.6 KD PROTEIN.;
6157	15115	24858	3.7	1.6E-01	AW291215.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN.;
6571	16429	26612	1.84	1.6E-01	AW246359.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
6592	16472	26662	1.42	1.6E-01	L49349.1	NT	HYPOTHETICAL 127.6 KD PROTEIN.;
7187	17064	27254	1.89	1.6E-01	Z49501.1	NT	HYPOTHETICAL 127.6 KD PROTEIN.;
7564	17415		1.7	1.6E-01	BF375171.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
7565	17416	27631	1.91	1.6E-01	Z49501.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8049	17940	28190	2.71	1.6E-01	AW850853.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8364	18241	28490	1.78	1.6E-01	O14947	SWISSPROT	UI-H-B12-agi-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
8364	18241	28491	1.78	1.6E-01	O14947	SWISSPROT	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8459	18332		7.6	1.6E-01	AF106064.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8713	18530	28814	10.07	1.6E-01	6671552	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9001	18804	29097	2.69	1.6E-01	AW877127.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
9025	19678		2.17	1.6E-01	6679466	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9141	18896	28795	2.33	1.6E-01	AV719585.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
9565	19493		6.33	1.6E-01	AB045310.1	NT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
9727	19265		2.84	1.6E-01	AK024496.1	NT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
							Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
							Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
							QV2-PT010-160400-133-a08 PT010 Homo sapiens cDNA
							Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
							AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
							Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
							Homo sapiens mRNA for FLJ00104 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	19319		2.47	1.5E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19328	25208	1.27	1.5E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
248	10214	20030	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	10697	20534	1.4	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1076	10992	20834	0.88	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1081	10997	20838	1.87	1.5E-01	AJ251885.1	NT	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11708	20953	1.36	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1254	11161	21010	2.81	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1254	11161	21011	2.81	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1866	11762	21636	1.54	1.5E-01	AW444451.1	EST_HUMAN	UI-H-BI3-akb-b-09-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2679	12544	22435	1.12	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2999	12927	22719	0.89	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22	1.5E-01	AA95049.1	EST_HUMAN	cc68d05.s1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3322	13242	23048	0.87	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3322	13242	23049	0.87	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3380	13298	23097	0.96	1.5E-01	AW612237.1	EST_HUMAN	hh29f02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2955539 3' similar to contains element MER16 repetitive element;
3696	13610	23394	1.34	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35	1.5E-01	AW565983.1	EST_HUMAN	h10106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	13718	23506	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3806	13718	23507	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3964	13871	23649	0.96	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4006	13912	23687	0.97	1.5E-01	Z12628.1	NT	B.napus mitochondrion DNA for ORF158
4091	13991	23768	8.36	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24301	1.34	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4645	12544	22435	2.18	1.5E-01	BF695381.1	EST_HUMAN	602083259P1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4680	14566	24361	1.08	1.5E-01	BE173790.1	EST_HUMAN	CM0-H10565-280200-245-b10 HT0565 Homo sapiens cDNA
4680	14566	24362	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-H10565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14808	24576	1.3	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.94	1.5E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	15139	24833	2.02	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5266	15188						SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5400	15319	25367	5.97	1.5E-01	P15196	SWISSPROT	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5424	15345	25308	4.06	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5424	15345	25399	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5652	15564	25660	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5652	15564	25661	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5684	15593	25694	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5760	15668	25774	1.37	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5785	15691		2.44	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3633981 5'
			1.66	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5828	15734	25845					Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5917	15945	25948	1.78	1.5E-01	AF134907.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5935	15840	25963	1.96	1.5E-01	AE001039.1	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
			5.13	1.5E-01	11417238	NT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5942	15847	25971					AMELOGENIN
5972	15876	26000	1.81	1.5E-01	P48508	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6031	15935	26067	2.09	1.5E-01	Q28462	SWISSPROT	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
6166	15123	24866	1.4	1.5E-01	P30143	SWISSPROT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6284	16148		5.63	1.5E-01	AW970295.1	EST_HUMAN	wr52c08.x1 NCJ_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
6374	16236	26396	1.77	1.5E-01	AF210842.1	NT	UI-HF-BNO-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26507	1.88	1.5E-01	A1973157.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.98	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
			1.68	1.5E-01	AW500611.1	EST_HUMAN	oo85g12.s1 NCJ_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1673030 3' similar to gb:M26062
6786	16665	26856					INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
6895	16774		1.22	1.5E-01	AA970317.1	EST_HUMAN	CT6800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
6912	16790	26983	11.77	1.5E-01	CI6800.1	EST_HUMAN	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
6996	16873	27064	1.88	1.5E-01	U27835.1	NT	Homo sapiens mRNA for ASK1, complete cds
			1.44	1.5E-01	D84476.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	17007	27200	1.71	1.5E-01	4301972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
7265	17142	27335	2.48	1.5E-01	N74226.1	EST_HUMAN	z559a06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
7305	17182		2.98	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7706	17556	27781	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7706	17556	27782	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X98852.1	NT	P. leniusculus mRNA for integrin beta subunit
7908	17758	27998	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7908	17758	27999	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7939	17789	28031	1.54	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
8009	17859	28103	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8009	17859	28104	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8199	18084	28334	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8199	18084	28335	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8342	18219		1.74	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
8425	18299	28555	1.73	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
8506	16236	26396	2.17	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
9099	19547		20.02	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
9531	19565		4.14	1.5E-01	R83077.1	EST_HUMAN	yp87s04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
9621	19588		2.14	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
9726	19497	25133	3.99	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
9832	19402	25179	3.01	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
9972	19432		1.58	1.5E-01	AF020346.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
296	10280		1.96	1.4E-01	AF008663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
892	10818		2.57	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1238	11145		1.62	1.4E-01	T91864.1	EST_HUMAN	y454c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	11615		1.43	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	11618	21487	1.53	1.4E-01	AE001710.1	NT	Thermoloba maritima section 22 of 136 of the complete genome
1893	11769		0.94	1.4E-01	AW135741.1	EST_HUMAN	UHF-B11-ecf-a-09-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	11837		10.35	1.4E-01	AA720615.1	EST_HUMAN	n72407.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2426	12303	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	12624	22517	3.07	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4083	13985	23762	8.38	1.4E-01	AI699094.1	EST_HUMAN	bx56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	23763	8.38	1.4E-01	AI699094.1	EST_HUMAN	bx56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
4313	14210		0.8	1.4E-01	AA776287.1	EST_HUMAN	zj50b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057.maf INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
5032	14904		0.91	1.4E-01	AW868022.1	EST_HUMAN	QV3-SN0022-100500-186-h09 SN0022 Homo sapiens cDNA
5116	14984	24759	1	1.4E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
5147	15014	24784	0.81	1.4E-01	AJ005180.1	NT	Lycopodium esculentum genomic RAPD band 26
5248	15171	24944	4.5	1.4E-01	T90577.1	EST_HUMAN	ye15c11.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5267	15189	24903	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189	24904	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5805	15710	25823	2.72	1.4E-01	BE326891.1	EST_HUMAN	ht67c02.x1 NCL_CGAP_Kid17 Homo sapiens cDNA clone IMAGE:3133538 3'
5903	15809	25934	5.64	1.4E-01	AL117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	25935	5.64	1.4E-01	AL117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5958	15863	25985	3.07	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5969	15874		1.56	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537681 5'
5982	15887	26009	1.89	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
6371	16233		1.62	1.4E-01	AW015373.1	EST_HUMAN	UIH-B10-eat-c-09-0-UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6936	16814		1.33	1.4E-01	AV699047.1	EST_HUMAN	AV699047 GLC Homo sapiens cDNA clone GLCFSH06 3'
7167	17044	27236	4.48	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7300	17176	27377	8.05	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
7343	17211	27410	1.36	1.4E-01	W83411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
7387	17256	27461	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7387	17256	27462	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7436	16449	26639	2.03	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lal (IAL), and zinc finger protein (DNZ1) genes, complete cds
8091	17982		2.02	1.4E-01	AA811480.1	EST_HUMAN	oa99a03.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
8216	18100	28352	3.28	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NbHst Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	X65092.1	NT	C.perflingens ORF for putative membrane transport protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02	1.4E-01	X52102.1	NT	M. musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000890.1	NT	Ephydrata fluviatilis mRNA for aldolase, partial cds
9413	19065	25277	2.32	1.4E-01	X74773.1	NT	P. salina plastid gene secY
9427	19073		1.89	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
9560	19156		3.01	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
9646	19754		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19282		1.41	1.4E-01	BE782738.1	EST_HUMAN	601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3688795 5'
9831	19332		1.42	1.4E-01	11425031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19565		3.41	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
9926	19398		1.77	1.4E-01	AW377998.1	EST_HUMAN	MF0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281	20099	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
826	10753	20603	1.09	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20652	1.83	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20952	1.07	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1426	11331		1.36	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acidiphila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	12129		1.17	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49	1.3E-01	M66918.1	NT	Carassius auratus keratin type I mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.95	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolyolip, transacylase mRNA, complete cds
3661	13575	23362	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3661	13575	23363	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3667	13581	23368	0.78	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydroxyl dihydrogenase 4 [AKR1C4], exon 2
3714	13575	23362	0.86	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3714	13575	23363	0.86	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3734	13646	23431	0.85	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (fgg), mRNA
3906	13816		1.7	1.3E-01	AL151581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4046	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4066	13968		3.44	1.3E-01	AW36434.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4075	13977	23756	1.89	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4093	13993	23770	16.36	1.3E-01	AV273741.1	EST_HUMAN	x23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4192	14092	23870	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4192	14092	23871	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4218	14116		1.65	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4433	14328	24116	2.16	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4525	14418	24202	0.81	1.3E-01	BF679694.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
4771	15075		3.17	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'
4903	14783		0.86	1.3E-01	AL136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5074	14944	24718	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	14944	24719	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	15039	24805	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5173	15039	24806	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5292	15213	25013	2.51	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5428	15348		1.79	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5904	15810	25636	13.21	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5956	15861	25983	2.04	1.3E-01	X89891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6305	16169		2	1.3E-01	H48664.1	EST_HUMAN	y33402.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
6049	16529	26723	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6668	16548	26744	1.28	1.3E-01	BF690522.1	EST_HUMAN	6021870151F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
6858	16737		4.54	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YD1054c
6886	16765		4.14	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
6960	16838	27031	1.27	1.3E-01	BF690522.1	EST_HUMAN	6021870151F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
7452	17261	27467	4.45	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921		2.88	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
8444	18318	28577	1.83	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576	18444		5.13	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cfl2), mRNA
8873	18685	28976	3.72	1.3E-01	BE279449.1	EST_HUMAN	601159052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
9261	18966	25320	1.97	1.3E-01	BEG18346.1	EST_HUMAN	60146274F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
9399	19054		3.18	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
9757	19279		1.56	1.3E-01	AE026829.1	NT	Ephydraia fluviatilis mRNA for sALK-6, complete cds
9784	19297		1.32	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
9945	19414		1.26	1.3E-01	BF571764.1	EST_HUMAN	TR:060287 O60287 KIAA0539 PROTEIN. ;
							602078440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4263049 5'
378	10362	20185	7.21	1.2E-01	AI421744.1	EST_HUMAN	tf39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mna1
418	9985		1.55	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
535	10476		2.63	1.2E-01	AF039442.1	NT	Dictyostellium discoideum ORF DG1016 gene, partial cds
1355	11261	21117	2.78	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	11261	21118	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1361	11267		3.94	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
							AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1490	11395		1.13	1.2E-01	AA897474.1	EST_HUMAN	ai48a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
							Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1613	11517	21377	1.17	1.2E-01	Q14634	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1631	11535	21396	2.62	1.2E-01	AI285402.1	EST_HUMAN	NFAT3 (NF-ATC4) (NF-AT3)
1730	11631		29.48	1.2E-01	X89211.1	NT	qi69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1877	11773		1.43	1.2E-01	AW449368.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
2134	12022	21919	2.1	1.2E-01	BF248490.1	EST_HUMAN	UIH-BI3-akt-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2240	12124	22025	1.01	1.2E-01	AL163213.2	NT	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2546	12420	22310	2.02	1.2E-01	AW996556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2697	12561	22451	0.86	1.2E-01	AI623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive
2812	12741	22537	1.5	1.2E-01	U18018.1	NT	element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2872	12799	22594	1.96	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead colon HP1LRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2904	12831	22628	2.89	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
							Human creatine kinase-B mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.98	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	22923	2	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261099-021-d08 BT0259 Homo sapiens cDNA
3219	13143		0.97	1.2E-01	U67900.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350		0.79	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3477	13393	23198	1.14	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23199	1.14	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3704	13617		0.88	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4090	13990	23766	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4090	13990	23767	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
5012	14886		1.04	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5174	16040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5174	16040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5199	15062		2.47	1.2E-01	AW401836.1	EST_HUMAN	UI-HF-BK0-aah-d-01-q-U1r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617 5'
5251	16174	24947	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_perathryoid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5297	16218	25021	1.9	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5762	15669	25776	1.69	1.2E-01	BE620946.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
5806	15711	25824	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
5839	15745	25858	1.56	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6607	16487		1.21	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
6642	16522	26715	2.46	1.2E-01	A1913753.1	EST_HUMAN	wc99g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
6893	16772		9.72	1.2E-01	AW083652.1	EST_HUMAN	Q99735 MICROSMAL GLUTATHIONE S-TRANSFERASE II ; xc49d07.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
6904	16782		3.86	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
7043	16920		2.27	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
7521	17340	27546	1.5	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
8260	18140		2.95	1.2E-01	D26184.1	NT	Yeast MF-T5 gene for suppressor protein, complete cds
8417	18291		3.35	1.2E-01	BE962324.2	EST_HUMAN	60165578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
8487	18360		1.93	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8579	18447	28715	2.6	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	18612		2.02	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822		2.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCF1B12 3'
9383	19043		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
9458	19693		2.58	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
9567	10476	24897	7.69	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19230		1.41	1.2E-01	X33981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
9739	19706	24903	2.36	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9761	19281	25231	3.68	1.2E-01	A1299603.1	EST_HUMAN	qn20g05.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9782	19295		2.07	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19636		4.72	1.2E-01	O96433	SWISSPROT	CYCLIN T
9960	19424		2.18	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
552	10493	20301	0.95	1.1E-01	A1561003.1	EST_HUMAN	In1808.x1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:2167983 3'
599	10535	20344	3.38	1.1E-01	AA699006.1	EST_HUMAN	nm08g11.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:4286771 5'
1038	10956	20759	1.53	1.1E-01	BF997308.1	EST_HUMAN	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1069	10985		1.29	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1143	12886	20899	4.06	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGe resequences, MAGL Homo sapiens cDNA
1229	11137	20690	1.72	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
1504	11408	21267	2.47	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLAGE2 Homo sapiens cDNA clone PLACE2000403 5'
2266	12150		2.25	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptoia), mRNA
2492	12653		1.17	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2520	12394		1.17	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2825	12754	22546	1.84	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [Hnca, Genomic, 700 nt, segment 4 of 5]
2997	12925	22717	0.8	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3299	13221		1.39	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca α 1g), mRNA
3374	13293	23092	3	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3405	13322	23123	1.54	1.1E-01	X52135.1	NT	C. reinhardtii nuclear gene on linkage group XIX
3534	13450	23246	0.94	1.1E-01	Y07695.1	NT	A. immersus gene for transposase
3648	13562	23348	1.23	1.1E-01	X52708.1	NT	G. gallus gene encoding non-histone chromosomal protein HMg-14b, exons 4 and 5
4021	13925	23698	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4021	13925	23699	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930		0.87	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
4159	14059		7.93	1.1E-01	AF157066.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
4189	14089	23867	0.8	1.1E-01	AW802056.1	EST_HUMAN	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4466	14360	24150	0.91	1.1E-01	AF054564.2	NT	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4539	14432	24214	2.02	1.1E-01	S44957.1	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4725	14611	24397	1.26	1.1E-01	Y07695.1	NT	Tapa-1= integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4819	14702	24487	1.25	1.1E-01	D90908.1	NT	A. immersus gene for transposase
5479	15399		1.43	1.1E-01	AA747216.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
5562	15478	25551	1.54	1.1E-01	X38851.1	NT	mx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element ;
5579	15494	25570	4.73	1.1E-01	M86533.1	NT	S. pombe sle8 gene encoding protein kinase
5672	15581	25681	1.46	1.1E-01	AJ007973.1	NT	Providencia rettgeri penicillin G amidase gene
5687	15596	25697	1.79	1.1E-01	BE769152.1	EST_HUMAN	Homo sapiens LGMD2B gene
5697	15606	25708	7.01	1.1E-01	AW853699.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5876	15782	25903	1.39	1.1E-01	AF035746.1	EST_HUMAN	RC3-CT0254-280399-011-a01 CT0254 Homo sapiens cDNA
5985	15890	26012	3.48	1.1E-01	O69835	SWISSPROT	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6027	15931		2.9	1.1E-01	AF032922.1	NT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6068	16052	26198	2.21	1.1E-01	11432372	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6448	16309	26474	7.05	1.1E-01	BF684628.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6448	16309	26475	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6513	16372	26550	1.74	1.1E-01	P41067	SWISSPROT	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6531	16390	26570	3.07	1.1E-01	AA788784.1	EST_HUMAN	TRAB PROTEIN
6777	16656	26845	1.57	1.1E-01	AA493574.1	EST_HUMAN	af31b06.s1 Soares parathyroid tumor_NH-IPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
6777	16656	26846	1.57	1.1E-01	AA493574.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
6803	16682	26872	1.22	1.1E-01	X91233.1	NT	ph04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6826	16705		1.24	1.1E-01	AW817918.1	EST_HUMAN	ph04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6862	16741	26934	1.78	1.1E-01	AL134349.1	EST_HUMAN	H. sapiens IL15 gene
7118	16995	27186	2.19	1.1E-01	U02482.1	NT	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
							DKF7p547P194_r1 547 (synonym: hfor1) Homo sapiens cDNA clone DKF7p547P194 5'
							Pedococcus acidiactici H plasmid pSMB74 pedocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294	2.24	1.1E-01	AA192153.1	EST_HUMAN	zpb3b12.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7228	17105	27295	2.24	1.1E-01	AA192153.1	EST_HUMAN	zpb3b12.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7287	17163	27362	2.48	1.1E-01	T72675.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
7467	17327		2.08	1.1E-01	BF085149.1	EST_HUMAN	gb1M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7861	17711		1.23	1.1E-01	R80590.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
8181	12925	22717	1.94	1.1E-01	F03265.1	EST_HUMAN	y96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
8294	18173		3.88	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
8402	18278	28530	2.93	1.1E-01	R23708.1	EST_HUMAN	Carassius auratus actvln beta A precursor, mRNA, complete cds
8519	18391	28655	1.95	1.1E-01	X70058.1	NT	y135f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
8539	18411	28676	3.21	1.1E-01	Z11910.1	NT	M.musculus cytokine gene
8539	18411	28677	3.21	1.1E-01	Z11910.1	NT	Z.nobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8626	18491	28763	2.79	1.1E-01	P17437	SWISSPROT	Z.nobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
9241	18956		3.19	1.1E-01	BE767023.1	EST_HUMAN	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9485	19507		2.06	1.1E-01	BE974566.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
9893	19372	25192	2.14	1.1E-01	BF239753.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
1183	11094		4.08	1.0E-01	O62855	SWISSPROT	601906360F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134985 5'
1251	11158	21007	1.89	1.0E-01	A1985499.1	EST_HUMAN	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1370	11276	21132	2.88	1.0E-01	AL161504.2	NT	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.f3 MER7 repetitive element;
2439	12316	22213	1	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3468	13384	23189	0.98	1.0E-01	BF033991.1	EST_HUMAN	UI-H-B13-alc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3658	13572	23359	1.01	1.0E-01	BF239818.1	EST_HUMAN	601458301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3871	13782	23574	2.44	1.0E-01	BF365703.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4307	14204	23987	1.5	1.0E-01	AE002265.2	NT	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4455	14349		1.17	1.0E-01	AI792349.1	EST_HUMAN	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4613	14501	24289	1.26	1.0E-01	U50450.1	NT	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4838	14719	24502	2.06	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5158	15025	24792	0.87	1.0E-01	D49883.1	NT	EST364414 MAGe resequences, MAGB Homo sapiens cDNA
5188	15051	24815	1.44	1.0E-01	BF515335.1	EST_HUMAN	Mouse FTZ-F1 gene
5260	15182		9.16	1.0E-01	W86490.1	EST_HUMAN	UI-H-BW1-aca-e-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3'
5670	15580	25680	11.21	1.0E-01	AF274875.1	NT	zh62h04.s1 Soares fetal liver spleen 1NfLS S1 Homo sapiens cDNA clone IMAGE:416695 3' Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072		1.88	1.0E-01	R23821.1	EST_HUMAN	yf34h06.r1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
6549	16407		2.45	1.0E-01	Y12488.1	NT	M.musculus whn gene
7299	17175	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synemon mRNA, complete cds
7473	17333		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori strain J99 section 62 of 132 of the complete genome
7651	17501	27724	1.84	1.0E-01	BF240154.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17563	27788	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7713	17663	27789	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	28007	1.26	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
8050	17941		2.02	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYROT1 Homo sapiens cDNA clone THYROT1000895 3'
8393	18269	28520	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8393	18269	28521	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
9703	18521	28803	4.43	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
9226	19285		2.5	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
9453	19085		1.34	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
9469	19099		2.03	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
9735	19888		2.57	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9765	19285		2.46	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
9818	19664		8.59	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9871	19360	25187	1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for Tcc34-2 protein (tcc34B gene)
9877	19363		4.16	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2752	12614	22505	1.09	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2757	12619	22511	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2757	12619	22512	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2950	12877	22675	0.92	9.9E-02	AV730747.1	EST_HUMAN	AV730747 HTF Homo sapiens cDNA clone HTFEND05 5'
3229	13153	22952	1.15	9.9E-02	AF09810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
4582	14472	24280	22.55	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCLGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6161	15118	24862	7.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7332	17236	27440	1.5	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
551	10492		1.58	9.8E-02	X56338.1	NT	O.sativa RAmly3C gene for alpha-amylase
1711	11612	21482	1.53	9.8E-02	4503224	NT	Homo sapiens cytochrome P450, subfamily 1F, polypeptide 1 (CYP2F1) mRNA
3106	13032	22827	3.28	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	23805	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4131	14031	23806	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
8755	17904	28148	2.1	9.8E-02	EF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
1328	11235	21092	1.16	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3901	13811		3.56	9.7E-02	Q69796	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5661	15572	25669	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 IMAGE resequences, MAGC Homo sapiens cDNA
6321	16184	26345	4.27	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
6655	16535	26731	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
6655	16535	26732	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7137	17014	27207	1.32	9.7E-02	A1953984.1	EST_HUMAN	wx78b06.x1 NCL CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
8531	18403		1.97	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
1969	11862	21763	1.27	9.6E-02	A1080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
1969	11862	21754	1.27	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4248	14147	23921	6.02	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4932	14810	24579	0.94	9.6E-02	AW966230.1	EST_HUMAN	Protein mirabilis fimbrial operon, strain HI4320
5093	14963	24738	0.8	9.6E-02	BE061729.1	EST_HUMAN	EST378303 IMAGE resequences; MAGC Homo sapiens cDNA
5713	15621		2.72	9.6E-02	BE910039.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
7502	17371	27560	1.51	9.6E-02	AV687898.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone GKCAH-02 5'
7677	17527		1.84	9.6E-02	BE984895.1	EST_HUMAN	AV687898 GKGO Homo sapiens cDNA clone GKCAH-02 5'
7772	17622	27855	1.76	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3900165 5'
7772	17622	27856	1.75	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumor suppressor gene, exons 1 to 55
7839	17689	27933	1.59	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumor suppressor gene, exons 1 to 55
7839	17689	27934	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tan3 pseudogene for transposase (in S-5 copy)
7886	17736	27980	3.29	9.6E-02	P08174	SWISSPROT	Antirrhinum majus transposon Tan3 pseudogene for transposase (in S-5 copy)
8125	18013	28260	6.51	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
8957	18764	29056	1.8	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
9798	19312		1.38	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
9848	19344	25212	1.26	9.6E-02	BE728219.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'
4012	13918	23694	2.25	9.5E-02	AW992395.1	EST_HUMAN	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3632908 5'
5062	14932	24704	0.87	9.5E-02	U63374.1	NT	OM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
							Lycopodium esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6323	16186	26348	3.72	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
6467	16327	26494	7.46	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
6599	16479	26666	2.59	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
6599	16479	26667	2.59	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28206	3.29	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28207	3.29	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1792	11690	21565	3.86	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1820	11717	21597	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	11717	21598	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13716	23504	4.34	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
4980	14855	24621	0.89	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdbp), mRNA
6999	16876		2.62	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, migA, ORF2 and ORF3 genes
8304	16338	26505	2.69	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and ipf35 gene, partial cds
9083	19603		3.36	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
9943	19411	25182	1.42	9.4E-02	U27699.1	NT	Human pepHGT-1 betaine-GABA transporter mRNA, complete cds
2960	12887		1.83	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2993	12921		5.39	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3218	13142	22946	2.03	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4060	13962	23738	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4060	13962	23739	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4628	14516		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
7599	17450	27665	2.24	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
7855	17705	27949	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7855	17705	27950	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7913	17763		3.74	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B1-afx-h-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
9704	19555		8.62	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr
9896	19602		1.95	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20008	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20009	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20010	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2180	12067		2.2	9.2E-02	R54156.1	EST_HUMAN	y98f07.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22866	4.53	9.2E-02	Q28631	SW/ISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3285	13188	22986	1.16	9.2E-02	AA534354.1	EST_HUMAN	m79e01.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3537	13453		1.12	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
4145	14045		1.34	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4538	14431	24213	1.86	9.2E-02	X96402.1	NT	G.gallus Mia-CK gene
6670	16550	26746	1.86	9.2E-02	T49920.1	EST_HUMAN	ya99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823	2.07	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
417	9984	19776	2.77	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
2365	12245	22139	1.01	9.1E-02	P78985	SW/ISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3618	13532		1.14	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4383	14279	24056	1.81	9.1E-02	AL151554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25487	1.73	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6372	16234	26393	11.89	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7958	17808		1.65	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
9021	18815		1.29	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
9256	19692		1.52	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611763 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
9785	19548		5.63	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	10659	20490	3.36	9.0E-02	P15328	SW/ISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1617	11521	21379	6.45	9.0E-02	BE220482.1	EST_HUMAN	hva9g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2772	12634	22528	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22529	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3294	13216	23018	0.92	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4202	14101	23883	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23884	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4321	14218	24001	1.2	9.0E-02	P55268	SW/ISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4568	14460	24248	1.79	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	15009	24780	1.06	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZEST1
5647	15560	25653	8.02	9.0E-02	W56037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
9967	19428		15.35	9.0E-02	11431759	NT	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21189	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1419	11325	21190	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2338	12218	22117	1.41	8.9E-02	BE15372.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	AF288055.1	NT	Atrichum angustatum AtranFio2 protein (AtranFio2) gene, partial cds
4534	14427	24208	0.92	8.9E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
5569	15485	25559	3.3	8.9E-02	AW452122.1	EST_HUMAN	UIH-B13-alo-f08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5569	15485	25560	3.3	8.9E-02	AW452122.1	EST_HUMAN	UIH-B13-alo-f08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5576	15491	25568	3.13	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
6270	16135	26290	1.56	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320		1.83	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
6998	16875	27066	5.28	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949		4.03	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1351	11257	21113	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	23532	0.96	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
3948	13856		3.24	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4205	14704		1.13	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7195	17072	27260	1.83	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
8461	18334	28596	3.19	8.8E-02	BE294455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8461	18334	28597	3.19	8.8E-02	BE294455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8585	18453	28722	10.63	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
9302	19001	25332	1.38	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
3636	13550	23337	3.02	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq26STS protein (XQ26ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338	3.02	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq26STS protein (XQ26ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3879	13790	23578	0.82	8.7E-02	W87841.1	EST_HUMAN	zh68a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element:
4609	14497	24286	1.22	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.06	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1175181 to 1189406 (section 101 of 148) of the complete genome
5255	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
8094	17985		2.58	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
8631	18496	28770	1.77	8.7E-02	AJ007763.1	NT	Glucanobacter oxydans RNA-III and RNA-IIIa genes
9293	18994		2.58	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9484	19105		1.81	8.7E-02	6879057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1232	11139	20991	7.05	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2197	12084	21986	2.22	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3151	13076	22876	2.94	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3593	13507		3.07	8.6E-02	AF153362.1	NT	Dicystotellum discoideum adenylyl cyclase (acrA) gene, complete cds
4385	14281	24060	0.87	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5708	15616	25718	4.38	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
5846	15752	25857	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
5846	15752	25858	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
9628	16508	26695	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
6628	16508	26695	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8315	18192	28441	1.98	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192		1.98	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8674	18442	28442	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8574	18442	28711	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8738	17887	28131	4.71	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
8858	18670	28958	1.73	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2347	12227	22124	2.87	8.5E-02	AE000552.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5500	15419		1.8	8.5E-02	P08089	SW/ISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5668	15570	25665	5.34	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7003	16880	27072	1.93	8.5E-02	6764779	NT	Mus musculus myosin XV (Myo15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7661	17511	27738	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
8498	18369		11.15	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
8512	18384	28649	4.07	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9681	19488		1.39	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9841	19339		3.28	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2632	12728	22391	4.24	8.4E-02	W69330.1	EST_HUMAN	z444e1.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5253	15175	24949	7.82	8.4E-02	BE267153.1	EST_HUMAN	601190439F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5'
8019	16923	26053	1.71	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6680	16560	26755	8.11	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
7931	17781	28020	1.44	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
1965	11859	21748	0.86	8.3E-02	5835680	NT	O88312 GOB-4. ;
1965	11859	21749	0.86	8.3E-02	5835680	NT	ixodes hexagonus mitochondrion, complete genome
3544	13460	23254	6.19	8.3E-02	P76334	SWISSPROT	HYPOHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	13481	23271	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3567	13481	23272	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5840	15746	25859	2.82	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6653	16533	26728	3.42	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drip2) mRNA, complete cds
6671	16551		1.47	8.3E-02	AA865285.1	EST_HUMAN	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1
6829	16708		1.42	8.3E-02	AA987873.1	EST_HUMAN	repetitive element ;
7498	17368	27573	1.44	8.3E-02	AW583503.1	EST_HUMAN	og81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
7506	17294		1.94	8.3E-02	AL161595.2	NT	la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9307	16695		1.55	8.3E-02	BE988488.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
1357	11263		7.82	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1480	11385	21248	1.21	8.2E-02	AF167077.2	NT	601644770F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:3929993 5'
3036	12964		1.78	8.2E-02	AL163206.2	NT	Gallus gallus mRNA for OBGM protein gamma isoform
3733	13645		1.26	8.2E-02	AL161498.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3926	13835	23615	1.11	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23862	5.36	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4187	14087	23863	5.36	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23864	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	24655	2.82	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5271	15193	24908	1.43	8.2E-02	BE997030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6188	16073	26222	3.14	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
7636	17387	27598	5.33	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
7628	17479	27699	2.11	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355586 5'
9314	19006	25336	4.13	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
9706	19480		1.84	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11394	21247	1.72	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
7703	17553		1.65	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
8789	18604	28594	3.38	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	12857	19784	3.28	8.0E-02	AW954653.1	EST_HUMAN	EST366723 IMAGE resequences, MAGC Homo sapiens cDNA
920	10844	20890	1.33	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1671	12701	21440	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1671	12701	21441	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1861	11757	21832	3.9	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2323	12204	22103	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2323	12204	22104	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2421	12298		4.08	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2790	10991	20833	0.81	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2870	12797	22591	1.01	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3745	13658	23440	0.84	8.0E-02	AW965118.1	EST_HUMAN	EST378191 IMAGE resequences, MAGI Homo sapiens cDNA
3980	13837		1.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4709	14595		5.62	8.0E-02	X72794.1	NT	Mus musculus gene for gelatinase B
4834	14716	24499	0.87	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (uRNAs)
5591	15506	25581	3.35	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6261	15506	25581	1.63	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6727	16307	26798	3.65	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7401	17268	27471	1.49	8.0E-02	X74208.1	NT	H sapiens AGT gene, intron 4
7401	17268	27472	1.49	8.0E-02	X74208.1	NT	H sapiens AGT gene, intron 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	26300	2.94	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
9881	13887		1.47	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9989	19654		3.04	8.0E-02	AJ278435.1	NT	Mus musculus Ranbp7 gene, Staf gene and Wee1 gene
2127	12015	21913	3.98	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2989510 5'
2948	12875	22673	6.43	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3776	13688	23471	3.31	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4695	14483	24269	1.06	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4706	14592		1.16	7.9E-02	AB008019.1	NT	602019770F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5'
6682	16562	26756	3.25	7.9E-02	U27832.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
7762	17612	27838	5.68	7.9E-02	AI081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Smi4p (SMI4) gene, complete cds
7762	17612	27839	5.68	7.9E-02	AI081644.1	EST_HUMAN	cu63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1192	11102	20947	1.43	7.8E-02	AF793275.1	EST_HUMAN	CE08811 ;
1192	11102	20948	1.43	7.8E-02	AF793275.1	EST_HUMAN	CE08811 ;
4688	14574	24371	0.81	7.8E-02	BE83633.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
5019	13603		2.71	7.8E-02	BE250048.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5197	15060	24825	1.04	7.8E-02	AI418520.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7236	17113	27306	2.06	7.8E-02	AF233437.1	NT	repetitive element ;
7236	17113	27307	2.06	7.8E-02	AF233437.1	NT	repetitive element ;
7389	17307	27513	1.27	7.8E-02	AA469354.1	EST_HUMAN	PM3-FN0058-140700-005-09 FN0058 Homo sapiens cDNA
1378	12693	21139	1	7.7E-02	AF181897.1	NT	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
3638	13454		2.09	7.7E-02	AJ238093.1	NT	tg48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element ;
6615	16495	26682	4.4	7.7E-02	AA402949.1	EST_HUMAN	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
						NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
						NT	nc68b05.r1 NCI_CGAP_Prt1 Homo sapiens cDNA clone IMAGE:771731
						EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
						NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
						NT	zu53d11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
						EST_HUMAN	TR:G1173905 G1173905 SPLICESOME ASSOCIATED PROTEIN. ;

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7680	17510	27736	4.62	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
8376	18253	28504	5.24	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
9535	19561		2	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3362	13281	23081	0.94	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' and similar to similar to protocadherin 43
3512	13428	23229	0.93	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.96	7.6E-02	AW85844.1	EST_HUMAN	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
7383	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
7695	17545		1.34	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
8927	18736	28028	2.45	7.6E-02	AW996646.1	EST_HUMAN	QV3-BN0046-150400-151-a04 BN0046 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20536	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4407	14301	24085	0.84	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
6855	16734	26927	1.19	7.5E-02	AJ894367.1	EST_HUMAN	w152b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
6953	16831	27024	1.21	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA100264 5'
469	10412	20231	1.23	7.4E-02	AW638547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1444	11349		1.08	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	12410		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3545	13461	23255	0.89	7.4E-02	AB07885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2358385 3'
4606	14494	24282	3.38	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4687	14573	24370	2.66	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
4858	14738	24518	1.7	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
5913	15819		1.75	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
6612	16492	26678	1.4	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895284 5'
6950	16828	27021	1.37	7.4E-02	U66089.1	NT	Human peridic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9271	18975		2.08	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
9527	19674		2.82	7.4E-02	AW376431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
9678	19235	25242	1.81	7.4E-02	BF035099.1	EST_HUMAN	601453913F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
461	10405	20222	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

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461	10405	20223	0.96	7.3E-02	BE64961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	10603	20420	2.73	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1466	12695	21237	3.04	7.3E-02	AW900281.1	EST_HUMAN	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1801	12705		14.81	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	14806		1.01	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6413	16275	26437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6413	16275	26438	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16628		1.27	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8548	15788	25910	2.78	7.3E-02	AA79977.1	EST_HUMAN	224402.s1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19911	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	10093	19912	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1480	11365	21228	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1480	11365	21229	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12377		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3810	13722	23511	0.82	7.2E-02	AW296322.1	EST_HUMAN	U1-H-BWO-ajl-a-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4249	14148	23922	4.02	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4594	14482	24268	78.82	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
4997	14872	24636	0.94	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24922	3.03	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24923	7.62	7.2E-02	P11120	SWISSPROT	CALMODULIN
6252	16118	26272	9.33	7.2E-02	BF216086.1	EST_HUMAN	601863558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
6281	16145		1.75	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
7545	17396	27608	2.05	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUUG01 5'
7625	17476	27697	4.23	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
7749	17596	27818	2.64	7.2E-02	AW873187.1	EST_HUMAN	hc24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
7926	17776	28016	2.05	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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7983	17833	28073	5.47	7.2E-02	BE565003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
7994	17844		3.2	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
9178	18919	25346	1.44	7.2E-02	AA773696.1	EST_HUMAN	af51a04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
9214	18942		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
9273	18977		1.44	7.2E-02	AA584465.1	EST_HUMAN	no55h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
9332	19013		1.62	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
9346	19531		3.89	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
1862	11758	21633	1.65	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome
2247	12131	22028	5.08	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
9063	18844		4.98	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
517	10459	20270	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1484	11389		1.46	7.0E-02	X96977.1	NT	M.antiellia Mcut-1 gene
1725	11826	21495	1.36	7.0E-02	AA056343.1	EST_HUMAN	z166f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
2994	12922	22715	1.72	7.0E-02	AW138152.1	EST_HUMAN	UJ-H-B11-acy-c-07-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3822	13734	23523	1	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
3958	13866	23642	1.24	7.0E-02	BE070294.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4047	13949		1.08	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4121	14021	23759	1.27	7.0E-02	AF077821.1	NT	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4846	14727	24510	7.1	7.0E-02	BF381987.1	EST_HUMAN	Carls familiaris inducible nitric oxide synthase mRNA, complete cds
7259	17136	27329	1.25	7.0E-02	9828113	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7534	17385	27597	1.19	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
						NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
8679	18567	28850	2.39	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
503	10445	20256	5.34	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
503	10445	20257	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
						NT	Homo sapiens chromosome 21 segment HS21C010
1311	11217		1.31	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3724	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3724	13636	23422	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	14968		1.05	6.9E-02	AF079906.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6978	16855	27048	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
6978	16855	27049	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9208	18939		3.95	6.9E-02	X74315.1	NT	Xlaeis XFD2 mRNA for fork head protein
9385	19045		1.5	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFc HOMOLOG
9598	19180		2.19	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1839	11736	21610	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1839	11736	21611	1.11	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1865	11761	21635	3.91	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3062	12989	22780	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22781	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22782	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	14347		0.92	6.8E-02	BE141076.1	EST_HUMAN	MR0-H10069-071099-001-005 HT0069 Homo sapiens cDNA
6315	16178	26337	7.71	6.8E-02	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
6822	16701	26894	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
6822	16701	26895	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9011	19719		1.37	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
9140	18895		2.98	6.8E-02	AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
9764	19284		2.97	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1511	11416		2.17	6.7E-02	AF115536.1	NT	Oncothynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1851	11747	21622	2.5	6.7E-02	AI220285.1	EST_HUMAN	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3656	13570	23356	3.52	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
1326	11233	21089	1.05	6.6E-02	AI735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
1347	11253	21109	1.5	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2133	12021	21918	3.07	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3133	13058		1.32	6.6E-02	Q13555	SWISSPROT	MELATONIN-RELATED RECEPTOR (H9)
3418	13335	23139	8.61	6.6E-02	IR64306.1	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3432	13349	23154	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3432	13349	23155	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3989	13896	23673	1.58	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4904	14784	24558	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5167	15033	24800	1.34	6.6E-02	AF204882.1	NT	Amsacta albistriga nucleopolydnavirus AcORF17 homolog gene, complete cds
5190	15053	24817	0.84	6.6E-02	AE004345.1	NT	Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome
5968	15873	25998	3.09	6.6E-02	X06411.1	NT	P.vulgaris mRNA for chalcone synthase
6209	15869	26105	2.93	6.6E-02	AI24326.1	EST_HUMAN	qh41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
6635	16515	26706	1.48	6.6E-02	AF082572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7806	17656	27894	1.37	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
8330	18207	28457	6.28	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
9593	19175		2.08	6.6E-02	9937991	NT	Mus musculus DJPB gene (Djpb), mRNA
9882	19366		1.46	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
567	10506	20313	1.91	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
971	10895	20743	1.75	6.5E-02	7706088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1369	11276	21131	4.17	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1702	11603	21474	2.16	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5413	15333	25383	1.76	6.5E-02	AA443991.1	EST_HUMAN	zy46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038
8035	17927	28173	5.61	6.5E-02	AA185648.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
9034	18823		3.53	6.5E-02	M21496.1	NT	zr32g05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
9393	19051		3.73	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	10501	20307	1.53	6.4E-02	X94549.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
4802	12909	22708	1.35	6.4E-02	6996923	NT	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
5180	15044		8.78	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5346	15267	25094	1.4	6.4E-02	AI191956.1	EST_HUMAN	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5718	15825	25727	7.58	6.4E-02	AF052733.1	NT	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element ;
5718	15825	25728	7.58	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6079	16062	26210	5.23	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6853	16732		2.57	6.4E-02	6753323	NT	601680429R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7034	16911	27099	4.12	6.4E-02	AA093305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
7603	17454	27698	2.02	6.4E-02	AB011126.1	NT	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
							Homo sapiens mRNA for KIAA0554 protein, partial cds
8946	18754	29049	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	18754	29050	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9259	19635		3.65	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
9337	19017	25295	2.27	6.4E-02	AJ27174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1720	11621	21490					Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3552	13467		2.43	6.3E-02	AF109905.1	NT	HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17602	27825	2.09	6.3E-02	P37092	SWISSPROT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
8096	15637	25741	3.14	6.3E-02	AB010162.1	NT	601873316F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4097499 5'
9373	19039		3.29	6.3E-02	BF210736.1	EST_HUMAN	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4157	14057	23831	1.49	6.3E-02	P15276	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 68
4243	14142		3.37	6.2E-02	AL161572.2	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4479	14373		1.11	6.2E-02	AF271235.1	NT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4803	14687		5.41	6.2E-02	Q62191	SWISSPROT	AV705701 ADB Homo sapiens cDNA clone ADBB403 5'
7459	17319	27525	1.22	6.2E-02	AV705701.1	EST_HUMAN	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
8655	18544	28827	1.21	6.2E-02	6577898	NT	Meiarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
9129	19762		1.84	6.2E-02	AJ242735.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
9541	19142	25265	3.53	6.2E-02	AE000750.1	NT	7187108.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 5' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
256	10222	20038			BF112039.1	EST_HUMAN	Human mRNA, Xq terminal portion
3909	13819		1.98	6.2E-02	D16471.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
5150	15017	24785	4.53	6.1E-02	U73325.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
6809	16688	26877	2.65	6.1E-02	AB040897.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8112	18002	28248	1.01	6.1E-02	X99288.1	NT	IL3-H10618-110500-136-C06 H10618 Homo sapiens cDNA
9088	19670		5.44	6.1E-02	BE179543.1	EST_HUMAN	S japonicum mRNA for serine-enzyme
9783	19296		7.17	6.1E-02	X70939.1	NT	Homo sapiens chromosome 21 segment HS21C007
1241	11148	20997	3.6	6.1E-02	AL163207.2	NT	Thermoloba maritima section 89 of 136 of the complete genome
2641	12508	22399	1.41	6.0E-02	AE001777.1	NT	EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA
2745	12607		1.57	6.0E-02	AW968848.1	EST_HUMAN	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2906	10076	19892	1.61	6.0E-02	AB031289.1	NT	zp78c04.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2906	10076	19893	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3191	13116	22921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3583	13497		0.9	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5314	15235		3.46	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6172	15129	24848	2.86	6.0E-02	5174598	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6172	15129	24849	2.86	6.0E-02	5174598	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6265	16130	26284	1.97	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
6524	16383	26562	2.05	6.0E-02	A1204275.1	EST_HUMAN	qf58508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
7340	17208	27406	1.19	6.0E-02	A1623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
7340	17208	27407	1.19	6.0E-02	A1623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17278	27486	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
7411	17278	27487	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
9336	19016	25294	1.95	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
9715	19253		1.84	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
229	10198	20011	3.42	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
2965	12882	22681	2.59	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4770	14655	24443	0.88	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7008	16885	27077	1.87	5.9E-02	9055249	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
8165	18053		2.72	5.9E-02	6079870	NT	Mus musculus follistatin-like (Fstl), mRNA
8383	18260	28509	3.15	5.9E-02	11433356	NT	Homo sapiens ninein (LOC51199), mRNA
8842	18655		1.99	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
917	10841		4.35	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2830	12759		1.1	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3613	13527	23314	1.44	5.8E-02	AE001775.1	NT	Thermoboga maritima section 87 of 136 of the complete genome
4257	14156	23931	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4257	14156	23932	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132	4.21	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gbM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4447	14341	24133	4.21	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gbM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	14365		2.04	5.8E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6523	16382	26560	2.79	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
6523	16382	26561	2.79	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9227	18948		2.34	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
9518	19739		4.56	5.8E-02	AA604269.1	EST_HUMAN	h075ef1.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3018	12946	22738	1.34	5.7E-02	AI081944.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3033	12961	22754	1.34	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3731	13643	23428	1.8	5.7E-02	AW966791.1	EST_HUMAN	EST T378865 MAGI resequences, MAGI Homo sapiens cDNA
6740	16819	26808	1.42	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
8524	18396	28661	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
8524	18396	28662	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
9437	19558		5.55	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
9862	19630		2.47	5.7E-02	AF27490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
9796	19727		3.82	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1510	11415	21274	0.86	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4540	14433	24215	1.26	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4598	14486	24272	1.14	5.6E-02	AA290599.1	EST_HUMAN	Zs45c01.s1 NCL_CGAP_G051 Homo sapiens cDNA clone IMAGE:700416 3'
6008	15913	26040	4.74	5.6E-02	AW172708.1	EST_HUMAN	xj02c10.x1 NCL_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
6241	16107	26258	2.88	5.6E-02	BE080001.1	EST_HUMAN	QV0-BN0147-230400-214-g07 BN0147 Homo sapiens cDNA
7110	16987	27178	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7110	16987	27179	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7647	17497	27719	1.15	5.6E-02	AA482864.1	EST_HUMAN	n49d07.s1 NCL_CGAP_AV1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
8850	18862		2.18	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2618	12486	22375	8.16	5.5E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3179	13104	22809	3.6	5.5E-02	675550.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4777	14661	24448	0.81	5.5E-02	AF161266.1	NT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
5472	15392	25456	3.47	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5671	15392	25456	4.31	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6365	16228	26388	1.56	5.5E-02	6755902	NT	Mus musculus tuftelin 1 (Tuft1), mRNA
7566	17417	27632	1.3	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
7566	17417	27633	1.3	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
7619	17470	27689	1.48	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
8382	18259	28508	11.56	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
2986	12914		0.95	5.4E-02	AJ277468.1	NT	Oryza sativa tbb3-1 gene for putative Bowman Birk trypsin inhibitor
3375	15078		6.34	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4908	14787	24563	0.92	5.4E-02	U63528.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
5108	14976	24751	1	5.4E-02	M95761.1	NT	Mus musculus p-glycoprotein (mdrla) gene, exons 1 and 2
8083	17974	28223	1.79	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
9323	19552		1.56	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1037	10955	20797	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 S10213 Homo sapiens cDNA
1037	10955	20798	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 S10213 Homo sapiens cDNA
1489	11394	21255	18.21	5.3E-02	T94759.1	EST_HUMAN	ye37f12.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2447	12324	22222	3.14	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2912	12839	22638	3.91	5.3E-02	M59417.1	NT	Pseudomonas putida tggS gene
2912	12839	22639	3.91	5.3E-02	M59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3113	13038	22834	4.59	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4506	14399	24185	1.22	5.3E-02	AJ011048.1	NT	Pseudomonas putida tggS gene
5021	14894	24662	7.26	5.3E-02	M80463.1	NT	Arabidopsis thaliana eli5 gene, exons 1-11
5258	15180	24955	1.76	5.3E-02	AE000927.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5258	15180	24956	1.76	5.3E-02	AE000927.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6115	16009	26145	3.87	5.3E-02	AE000927.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6363	16216		1.94	5.3E-02	S78221.1	NT	Lymphocystis disease virus 1, complete genome
7276	17153	27349	1.78	5.3E-02	X03127.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
2239	12123		439.66	5.2E-02	5031903	NT	Podospora anserina mitochondrial epsilon-sen DNA
3076	13003	22793	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3076	13003	22794	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4181	14081	23854	3.35	5.2E-02	U07132.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4633	14521	24311	1.04	5.2E-02	L33246.1	NT	Human steroid hormone receptor Nrr-1 mRNA, complete cds
						NT	Drosophila melanogaster filament protein homolog (sepi) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5714	15622		1.73	5.2E-02	A830965.1	EST_HUMAN	wj80a04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
6768	16647		2.23	5.2E-02	AL163204.2	NT	MER15 repetitive element:
7610	17461	27677	2.03	5.2E-02	D10927.1	NT	Homo sapiens chromosome 21 segment HS21C004
7610	17461	27678	2.03	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9561	19157		1.63	5.2E-02	Q03030	SWISSPROT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
2313	12194		1.02	5.1E-02	AL134071.1	EST_HUMAN	Oxaloacetate decarboxylase ALPHA CHAIN
4979	14854	24620	1.12	5.1E-02	BE967423.2	EST_HUMAN	DKFZp547D073.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
6098	15108	24871	1.65	5.1E-02	BF378625.1	EST_HUMAN	601653565R2 NIH_MGC. 55 Homo sapiens cDNA clone IMAGE:3838361 3'
6959	16738	26930	1.43	5.1E-02	AF131666.1	NT	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
7645	17495	27716	6.22	5.1E-02	AF012898.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
7949	17699	27944	2.36	5.1E-02	P40603	SWISSPROT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
8204	18088	28339	2.42	5.1E-02	AF083930.1	NT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
8204	18088	28340	2.42	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
9559	19159		1.81	5.1E-02	AF082467.1	NT	Homo sapiens ES18 mRNA, partial cds
474	10418	20234	1.98	5.0E-02	AF098004.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
1186	11096	20942	7.11	5.0E-02	Z99104.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1947	11842	21726	4.27	5.0E-02	P02810	SWISSPROT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2788	10894	20742	1.64	5.0E-02	U72742.1	NT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
3295	13217		1.17	5.0E-02	7305610	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3929	13543	23330	5.53	5.0E-02	U12769.2	NT	Mus musculus Uroc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
4990	14770	24548	0.88	5.0E-02	AF188530.1	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6450	16311	26477	10.61	5.0E-02	P35616	SWISSPROT	Homo sapiens ubiquitous tetrapeptide containing protein RoXan mRNA, partial cds
7658	17708	27954	1.32	5.0E-02	AF305238.1	NT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
8762	18597	28986	2.47	5.0E-02	U67600.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
9096	19593		2.81	5.0E-02	Q04047	SWISSPROT	Methanococcus jannaschii section 142 of 150 of the complete genome
218	10788		28.95	4.9E-02	M14230.1	NT	NO-ON-TRANSIENT A PROTEIN
365	10321	20143	2.57	4.9E-02	AF275948.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
365	10321	20144	2.57	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3251	13174	22972	1.87	4.9E-02	P54258	SWISSPROT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3522	13438		0.87	4.9E-02	AA188940.1	EST_HUMAN	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3543	13469	23262	1.19	4.9E-02	AA400914.1	EST_HUMAN	zq48a12.s1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632826 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element:
							z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3543	13459	23253	1.19	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428.3'
4733	14618	24404	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386.3'
4733	14618	24405	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386.3'
5299	15220	25023	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5299	15220	25024	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
8705	18523	28805	3.78	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
9490	19107		2.26	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
9751	19276		3.67	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
327	10287	20104	1.46	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
328	10287	20104	1.97	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
480	10424	20239	7.54	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2227	12112	22014	1.92	4.8E-02	W51983.1	EST_HUMAN	z49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611.3' similar to gb-M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3172	13097	22903	2.12	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4572	14464		1.67	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
6076	14946	24722	1.28	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
6731	16611	26801	1.31	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-602 ST0129 Homo sapiens cDNA
4940	14818	24586	0.78	4.7E-02	6981261	NT	Rattus norvegicus Nesin (Nes), mRNA
6085	16030	26170	3.41	4.7E-02	W01153.1	EST_HUMAN	yz9709.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291017.5' similar to contains Alu repetitive element;
6134	15981	26117	1.65	4.7E-02	M62752.1	NT	Rat statin-related protein (st) gene, complete GDS
6800	16679	26868	9.71	4.7E-02	X15543.1	NT	B.taurus mRNA for RE-36-DNA-binding protein
7179	17056	27245	1.18	4.7E-02	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
7189	17066		2.63	4.7E-02	AB026676.1	NT	Gallus gallus Wpkci-8 gene, complete cds
7321	17197	27397	7.44	4.7E-02	X15543.1	NT	B.taurus mRNA for RE-36-DNA-binding protein
8136	18024	28270	1.76	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
9305	19740		2.35	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GJC Homo sapiens cDNA clone GICBKD02.3'
9652	19743		2.35	4.7E-02	P52951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
9881	19365		1.39	4.7E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
722	10654	20484	2.74	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1270	11177		1.06	4.6E-02	A014255.1	EST_HUMAN	am50402.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979.3' similar to TR:P90533 P90533 LIMA ;contains element L.TR1 repetitive element ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1336	11242	21100	2.74	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTC8WC01 5'
2438	12315	22212	2.51	4.6E-02	AW236023.1	EST_HUMAN	xn2403 x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN
2777	10235	20052	1.51	4.6E-02	BE163583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
2977	12904	22703	0.98	4.6E-02	BE163583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3451	12904	22703	0.96	4.6E-02	BE163583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4033	13936		1.22	4.6E-02	AF220385.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5777	15884	25792	3.64	4.6E-02	X61624.1	NT	Mus musculus nucleolar RNA helicase II(Gu (dxb21) gene, complete cds
5777	15884	25793	3.64	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6070	16053	26200	1.31	4.6E-02	A1149574.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
7029	16906	27097	3.65	4.6E-02	BE154006.1	EST_HUMAN	qc60b06.x1 Soares_placenta_80c9weeks_2Nbl-HF8tc9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element;
8707	18524	28806	3.58	4.6E-02	AA913328.1	EST_HUMAN	PM0-HT0339-080400-009-G12 HT0339 Homo sapiens cDNA
9633	19738		1.34	4.6E-02	L11692.1	NT	o27n09.s1 Soares_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
9845	19343		2.68	4.6E-02	X67808.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
439	10383	20207	1.84	4.5E-02	P22448	SWISSPROT	Human germine immunoglobulin lambda light chain gene
1200	11110	20955	0.85	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1200	11110	20956	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1763	11862	21535	3.55	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2063	11953	21850	2.04	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3662	13576	23364	3.83	4.5E-02	AL163278.2	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
5778	15885	25794	1.54	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6891	16770	26965	2.3	4.5E-02	AF036884.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7718	17688	27793	4.43	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
9301	19000	25331	1.74	4.5E-02	11418013	NT	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
9691	19637	25009	3.41	4.5E-02	AA191097.1	EST_HUMAN	Homo sapiens ret finger protein-like 3 (RFLP3), mRNA
213	10184		4.79	4.4E-02	BE972733.1	EST_HUMAN	2q43f11.t1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
1008	10926	20770	1.29	4.4E-02	L19295.1	NT	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2049	11940		6.15	4.4E-02	P31588	SWISSPROT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2440	12317	22214	1.29	4.4E-02	AW875475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3588	13502	23291	1.88	4.4E-02	AF159160.1	NT	QV2-P10012-070300-070-g02 PT0012 Homo sapiens cDNA
4827	14420	24203	1.08	4.4E-02	AF109907.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	14420	24204	1.08	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4637	14526		3.12	4.4E-02	AJ222889.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7084	16961	27184	1.96	4.4E-02	AA736989.1	EST_HUMAN	hw13h03.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
8423	18297	28552	4.11	4.4E-02	AF060699.1	NT	Hepatitis E virus strain HEV-US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
8533	18405	28670	2.39	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
9029	18820		1.88	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
9210	19753		1.44	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
764	10895	20532	5.74	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2521	12395	22286	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3383	13301	23101	7.04	4.3E-02	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3609	13523		1.07	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5141	16008	24779	0.92	4.3E-02	X51594.1	NT	Pea P4 organ specific gene
5914	15820	25944	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
5914	15820	25945	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
8242	18122	28372	2.48	4.3E-02	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
805	10734	20577	2.05	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
848	10775		1.93	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
878	10804	20654	0.83	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545684 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA; contains L1.13 L1 L1 repetitive element;
1690	11592		1.21	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment: 4/5
3117	13042	22838	0.9	4.2E-02	AI493472.1	EST_HUMAN	qy95f10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
5172	15038		1.07	4.2E-02	D63484.1	NT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); Human mRNA for KIAA0150 gene, partial cds
6444	16305	26470	4.45	4.2E-02	AF278752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7114	16991	27183	3.88	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7845	17695	27941	1.28	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
8627	18492	28764	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8627	18492	28765	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8795	18609	28900	1.73	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
9563	19681		2.69	4.2E-02	AI883494.1	EST_HUMAN	w49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2643	12510	22401	0.97	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3824	13736	23526	0.85	4.1E-02	DE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3824	13736	23527	0.86	4.1E-02	BE207236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4372	14268		7.37	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
6436	16297	26459	1.84	4.1E-02	7662347	NT	Homo sapiens KIA00867 protein (KIA00867), mRNA
6565	16423	26804	2.44	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
9873	19682	24994	12.83	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3206	13130	22932	2.68	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5304	15225	25029	4.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6528	16387	26567	5.69	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7059	16936	27126	2.8	4.0E-02	P08640	SW/SSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572	17423	27638	2.42	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
8983	18788		1.94	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
9196	19503	25135	4.96	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1104	11020	20863	2.77	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1322	11229	21084	3.46	3.9E-02	P41047	SW/SSPROT	FAS ANTIGEN LIGAND
1918	11813	21691	3.04	3.9E-02	AJ403366.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2671	12536		2.29	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5105	14973	24748	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5105	14973	24749	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
6581	16461	26654	1.22	3.9E-02	BF239613.1	EST_HUMAN	601900848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
9056	19644		5.45	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
9697	19248		1.57	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB reits, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
9811	19568		7.38	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmx28orf
1909	11804	21693	0.94	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
6331	16194	26355	1.74	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7033	16910		1.39	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
8045	17936	28185	2.45	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10899	20746	4.59	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	11272	21128	0.9	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	12077	21982	6.3	3.7E-02	A1984806.1	EST_HUMAN	wr85e08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2533	12407	22299	0.91	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3012	12940	22793	0.8	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3013	12941	22734	3.45	3.7E-02	BF312983.1	EST_HUMAN	601898233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125564 5'
3408	13325		1.1	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
9095	18867	29119	3.4	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
9755	19539	25063	1.62	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3604	13518	23306	0.85	3.6E-02	X73221.1	NT	H. vulgare Ssr1 gene for sucrose synthase
3612	13526	23313	0.8	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5135	15002	24773	0.84	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
6028	15932	26062	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6028	15932	26063	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6214	16080	26229	1.82	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt precursor (sgp2) gene, complete cds
6324	16187	26349	2.63	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb.J00314_rna2
7402	17269	27473	2.08	3.6E-02	U20608.1	NT	TUBULIN BETA-1 CHAIN (HUMAN); Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
877	10803	20693	1.15	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
992	10913	20758	1.53	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21309	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1544	11449	21310	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4120	14020	23798	2.01	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4220	14118	23895	1.43	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4536	14429		0.96	3.5E-02	AW958469.1	EST_HUMAN	EST370539 MAGC resequences, MAGC Homo sapiens cDNA
5154	15021		0.84	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
5773	15680	25787	1.88	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
7012	16889	27082	2.35	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
7755	17605	27829	1.72	3.5E-02	X76942.1	NT	L. lactis MG1363 grpE and dnaK genes
8785	18600	28889	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-281299-002-h03 CT0326 Homo sapiens cDNA
8785	18600	28890	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
9749	19582		3.51	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	10504	20310	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	10504	20311	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20310	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20311	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1035	10953	20795	3.77	3.4E-02	AW274020.1	EST_HUMAN	x26d07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211 HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1188	11098		10.22	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2343	12223	22120	2.05	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
3384	13302	23102	1.25	3.4E-02	AL163208.2	NT	HER29 repetitive element
3709	13622	23405	1.07	3.4E-02	BE839514.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3845	13756	23550	3.18	3.4E-02	AW794952.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4494	14388	24174	2.41	3.4E-02	X59799.1	NT	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4992	14867		3.43	3.4E-02	Q26457	SWISSPROT	M.musculus S-antigen gene promoter region
5010	14884	24650	1.28	3.4E-02	AJ012469.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6095	15105	24868	4.19	3.4E-02	U24993.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6808	16687		4.78	3.4E-02	A1869629.1	EST_HUMAN	Human lysyl oxidase-like protein gene, exon 3
							w199d04.x1 NCJ_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
							zq04f11.s1 Stragene muscle 937208 Homo sapiens cDNA clone IMAGE:628749 3' similar to
							TR:G1017425 G1017425
7169	17046		6.07	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEAENTLIN.KESVTADAGRYEITAANSSTGTTKAFINIVLDRPG
368	10324		13.18	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVV/SDITEESVTLKWEPPKYDGGQV/TNYLLKRETSJAVWTEVSA TVARTMMKVMKL ...;
1151	11064	20907	13.17	3.3E-02	AB035887.1	NT	P775e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1621	11525	21383	1.08	3.3E-02	AF110763.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
							Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1705	11806		1.28	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2038	11929		2.77	3.3E-02	R09112.1	EST_HUMAN	Y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4086	11525	21383	2.24	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4366	14262	24047	1.88	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
5875	15781	25901	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
5875	15781	25902	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8464	18337	28601	3.39	3.3E-02	BF691107.1	EST_HUMAN	60224717F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
9290	18991		1.78	3.3E-02	T96945.1	EST_HUMAN	ye49f11.1r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
9441	19078		1.59	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
127	10101	19923	1.13	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1110	11025	20867	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68), gene, hsp68d allele, complete cds
1110	11025	20868	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68), gene, hsp68d allele, complete cds
1734	11635	21503	1.14	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2072	11962		0.91	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2809	10101	19923	1.15	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3095	13022	22817	10.71	3.2E-02	BE867353.1	EST_HUMAN	60144243F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3653	13567	23354	1.05	3.2E-02	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	14024		12.36	3.2E-02	X94758.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4558	14544	24333	2.88	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5399	15318	25365	1.46	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stw gene
5399	15318	25366	1.46	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stw gene
5931	15836	25959	2.26	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
5932	15837		26.54	3.2E-02	T89367.1	EST_HUMAN	yc33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
5986	15891	26013	3.72	3.2E-02	AF173845.1	NT	Alu repetitive element; contains LTR1 repetitive element ;
6830	16709	26902	3.48	3.2E-02	6680565	NT	Saguinus oedipus tissue kallikrein gene, complete cds
7786	17636		3.82	3.2E-02	AA719795.1	EST_HUMAN	Mus musculus kinesin family member 3c (Kif3c), mRNA
9952	19487		1.38	3.2E-02	AB021694.1	NT	zg54b12.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1239	11146		2.05	3.1E-02	4503416	NT	gb1.08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1283	11191	21043	1.26	3.1E-02	P18945	SWISSPROT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
1850	11746	21621	1.35	3.1E-02	6671564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4), mRNA
1931	11826		1.09	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
							Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
							Drosophila melanogaster mRNA for headcase protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4152	14052		0.82	3.1E-02	AU119006.1	EST_HUMAN	AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
4767	14652	24440	0.99	3.1E-02	AW835313.1	EST_HUMAN	QV0-LT0014-250200-129-h09 LT0014 Homo sapiens cDNA
5290	15211		2.33	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
7765	17615	27843	2.62	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1606	11511		2.82	3.0E-02	AF187125.1	NT	Ptyokineins minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2541	12415	22305	1.07	3.0E-02	AA402242.1	EST_HUMAN	z65f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3518	13434	23234	1.07	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3603	13517	23305	2.61	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3685	13598		0.96	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
3666	13777		1.18	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
4773	14657	24444	0.89	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'
4983	14858	24624	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4983	14858	24625	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5312	15233		2.88	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6066	16050	26196	2.71	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6127	15974	26109	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6127	15974	26110	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6207	15967	26101	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6207	15967	26102	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6292	16156	26311	1.54	3.0E-02	M86524.1	NT	Human dystrophin gene
7106	16983		2.11	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
7978	17828	28089	1.71	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
8562	18432	28701	3.09	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8837	18745	29039	7.7	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
9396	19730	24909	1.66	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
9740	19273		4.67	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
9780	19723		2.09	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2385	12720	22157	1.1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2962	12889	22687	1.07	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2962	12889	22688	1.07	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3851	13762	23555	0.92	2.9E-02	H72805.1	EST_HUMAN	y07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4950	14827	24593	1.32	2.9E-02	X65137.1	NT	S.vulgaris pepC gene for PEP carboxylase
4950	14827	24594	1.32	2.9E-02	X65137.1	NT	S.vulgaris pepC gene for PEP carboxylase
5799	15705	25817	6.47	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
6298	16162	26319	10.33	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7568	17419	27635	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-P.T0014-071299-051-c04 P.T0014 Homo sapiens cDNA
7568	17419	27636	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-P.T0014-071299-051-c04 P.T0014 Homo sapiens cDNA
553	10494		0.87	2.8E-02	AW970153.1	EST_HUMAN	EST382234 IMAGE resequencing, MAGK Homo sapiens cDNA
3321	13241	23046	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3321	13241	23047	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4214	14112		0.98	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5373	15293	25140	11.41	2.8E-02	BE741063.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6847	16726	26920	1.33	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9874	19574		1.51	2.8E-02	R06986.1	EST_HUMAN	yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128675 5'
9880	19237		1.33	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S9A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
1473	11378	21242	1.26	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3385	13303	23103	2	2.7E-02	AL161494.2	NT	y66h12.r1 Soares multiple sclerosis_2Nb-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	14007	23783	2.07	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares multiple sclerosis_2Nb-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	14007	23784	2.07	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares multiple sclerosis_2Nb-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
6205	15965	26099	1.9	2.7E-02	AA993571.1	EST_HUMAN	cl96h03.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
9648	19500	25134	1.52	2.7E-02	BF514858.1	EST_HUMAN	U1-H-BW7-enj-f-05-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082520 3'
559	10499	20305	1.14	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1345	11251		1.04	2.6E-02	AW650515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2315	12196	22093	2.9	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2317	12198	22095	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2317	12198	22096	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
							Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2885	12812		1.55	2.6E-02	AF109906.1	NT	
3883	13794		1.13	2.6E-02	AW181945.1	EST_HUMAN	x66f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4517	14410		1.13	2.6E-02	BE969922.1	EST_HUMAN	601649977R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933786 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4811	14695	24481	3.69	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
4998	14873	24637	1.67	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5025	14898	24667	2.06	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCL_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5771	15678		6.95	2.6E-02	AI206030.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5870	15776	28895	2.08	2.6E-02	BE621748.1	EST_HUMAN	gg27f11.x1 NCL_CGAP_K183 Homo sapiens cDNA clone IMAGE:1762317 3'
6130	15977	28113	6.09	2.6E-02		EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885578 3'
7388	17306	27512	1.19	2.6E-02	698127.1	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7948	17798	28038	4.87	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
8692	18579		2.1	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8948	18660	28949	1.89	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.r1 NCL_CGAP_QGB1 Homo sapiens cDNA clone IMAGE:704162 5'
9320	19715	24906	1.55	2.6E-02	AW500347.1	EST_HUMAN	UI-HF-BN0-alk-e-10-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
521	10463	20274	1.45	2.5E-02	BF343827.1	EST_HUMAN	602015501F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150944 5'
521	10463	20275	1.45	2.5E-02	AI793130.1	EST_HUMAN	on28f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
792	10721	20562	12.83	2.5E-02	BE974314.1	EST_HUMAN	on28f06.y6 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1557827 5'
851	10778	20628	4.77	2.5E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2735	12597		2.59	2.5E-02	U12571.1	NT	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2926	12853	22652	4.4	2.5E-02	X99697.1	NT	Rattus norvegicus rebphilin-3A mRNA, complete cds
2926	12853	22653	4.4	2.5E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
3959	15070	23643	1.09	2.5E-02	BE701165.1	EST_HUMAN	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
3959	15070	23644	1.09	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4111	14011	23788	5.07	2.5E-02	AW592114.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
5759	15667		4.48	2.5E-02	BE670128.1	EST_HUMAN	hf36h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5767	15674		3.86	2.5E-02	BE746898.1	EST_HUMAN	7e30e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1
6519	16378	28555	1.57	2.5E-02	BF526722.1	EST_HUMAN	repetitive element ;
6519	16378	28556	1.57	2.5E-02	BF526722.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
8185	18071	28320	2.45	2.5E-02	Q10335	SWISSPROT	602070562F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
8185	18071	28321	2.45	2.5E-02	Q10335	SWISSPROT	602070562F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
8238	18118	28370	3.38	2.5E-02	AJ237936.1	NT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Bos taurus partial stat5B gene, exons 17-19
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (Ibeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp
8255	18135		3.33	2.5E-02	AF050157.1	NT	
8978	18783		1.74	2.5E-02	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9280	19657		2.19	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
9463	19628		1.63	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9881	19167	25271	2.39	2.5E-02	BE979327.1	EST_HUMAN	601652366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
167	10139	19956	1.89	2.4E-02	AI878882.1	EST_HUMAN	tc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1580	11484	21344	1.01	2.4E-02	H65884.1	EST_HUMAN	y75f11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1998	12710	21784	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1998	12710	21785	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4272	14171	23948	1.4	2.4E-02	J05110.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4420	14314	24099	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4420	14314	24100	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5119	14987		11.51	2.4E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6862	16840	27032	10.36	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294566 3' similar to
7643	17493	27714	2.17	2.4E-02	AY692954.1	EST_HUMAN	gbjK02909jRATSR7K Rat (rRNA), contains A3R.b1 A3R repetitive element ;
7734	17584	27808	2.98	2.4E-02	AA493894.1	EST_HUMAN	hh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
8857	18669	28956	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
8857	18669	28957	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
9080	18856		1.95	2.4E-02	9627809	NT	Bacteriophage b1L67, complete genome
9224	18947	25357	2.72	2.4E-02	6763635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
9282	18984	25326	2.03	2.4E-02	BE928869.1	EST_HUMAN	MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
9368	19036		1.27	2.4E-02	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9505	19120		3.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
9532	19138		1.6	2.4E-02	NA2980.1	EST_HUMAN	yy08a06.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270610 5'
9538	19141		1.38	2.4E-02	BF679477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
9977	19667		1.59	2.4E-02	P54643	SWISSPROT	SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN)
1829	11726		5.79	2.3E-02	W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:299294 5'
1844	11740		7.89	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2302	12183	22081	2.52	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3628	13542	23329	4.79	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADHP, Human foetal Brain Whole tissue Homo sapiens cDNA
4057	13959	23735	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4057	13959	23736	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4323	14220	24002	1.26	2.3E-02	AV989107.1	EST_HUMAN	CNA4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4347	14244	24027	0.81	2.3E-02	BE935225.1	EST_HUMAN	CN3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4347	14244	24028	0.81	2.3E-02	BE935225.1	EST_HUMAN	CN3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4348	15072	24029	0.94	2.3E-02	AV993693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4348	15072	24030	0.94	2.3E-02	AV993693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4472	14366	24155	1.75	2.3E-02	BE143160.1	EST_HUMAN	MRO-HT0159-151099-001-e03 HT0159 Homo sapiens cDNA
4490	14384	24171	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4490	14384	24172	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4948	14925	24591	1	2.3E-02	AI793177.1	EST_HUMAN	qz35d03.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
4948	14925	24592	1	2.3E-02	AI793177.1	EST_HUMAN	qz35d03.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
5302	15223	25027	3.57	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA
5990	15895	26018	4	2.3E-02	AL161505.2	NT	carboxylase beta chain (pccB) homolog gene, partial cds
6398	16478	26685	5.67	2.3E-02	U63610.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7764	17614	27841	1.51	2.3E-02	AE000199.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7764	17614	27842	1.51	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
							Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
							GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
8162	18050	28302	2.15	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE
9201	19512		4.41	2.3E-02	BE278331.1	EST_HUMAN	60117958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
9713	19254	25219	1.94	2.3E-02	U99394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
9767	19756		2.27	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
9961	19609		1.27	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
							Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
720	10652	20482	3.09	2.2E-02	AF018267.1	NT	Homo sapiens chromodomain helixase DNA binding protein 2 (CHD2) mRNA
1713	11614		1.53	2.2E-02	4557448	NT	S.pneumoniae pcpsA gene and open reading frames
1968	11861	21752	1.78	2.2E-02	Z62001.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
2695	12730	22448	1.4	2.2E-02	AF109633.1	NT	hn24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3388	13306		1.93	2.2E-02	AA577785.1	EST_HUMAN	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3595	13509		3.27	2.2E-02	AF083094.1	NT	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3779	13691	23477	1.05	2.2E-02	AW601317.1	EST_HUMAN	

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3844	13755	23549	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
6297	16161	26318	3.78	2.2E-02	AV669721.1	EST_HUMAN	AV669721 GKB Homo sapiens cDNA clone GKBAND03 3'
6876	16755	26952	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
6876	16755	26953	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7585	17436	27651	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7585	17436	27652	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9466	19096		2.24	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone MDSADG01 5'
413	10359		5.56	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
441	10385		7.99	2.1E-02	AF029726.1	NT	Dicotylestium discoideum histidine kinase C (dhkC) mRNA, complete cds
1242	11149	20998	7.43	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1365	11270	21125	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1365	11270	21126	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1920	11815	21694	0.95	2.1E-02	AF190899.1	NT	Tegula aureocincta major acrosomal protein precursor (TMAP) mRNA, complete cds
2785	10693	20530	3.98	2.1E-02	N29286.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:264541 5'
3110	11883	21776	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3110	11883	21777	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3335	13451	23247	1.23	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4038	13941	23719	0.89	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4342	14239	24022	1.61	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4351	14247	24033	1.03	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4611	14499	24288	4.65	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4714	14600	24386	0.86	2.1E-02	AB23432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
7553	17404	27618	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7553	17404	27619	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9449	15095		4.99	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
9557	19348	25184	3.33	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds
17	10004	19795	1.35	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3
18	10005	19796	7.86	2.0E-02	AW895565.1	EST_HUMAN	MER1 repetitive element; QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
259	10225	20040	2.63	2.0E-02	6753635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
292	10256	20077	2.62	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
781	10711	20550	1.75	2.0E-02	6753635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
1071	10987	20830	0.97	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[p36.33] of Homo sapiens
1181	11092	20936	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1181	11092	20939	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1830	11727	21600	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1830	11727	21601	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2768	12630		1.75	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3040	10004	19795	1.96	2.0E-02	BF002632.1	EST_HUMAN	7q57c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
3105	13031		1.16	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3189	13114		3.33	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3925	13834	23614	1.5	2.0E-02	MI18095.1	NT	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5079	14949	24725	0.99	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5085	14955	24730	0.99	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
7679	17629		1.8	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7930	17780	28019	1.59	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
8037	17929	28175	2.01	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
8678	18666	28849	2.55	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
8931	18739	29031	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
8931	18739	29032	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
9019	14955	24730	1.41	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
9481	12630		1.56	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9928	19536		1.72	2.0E-02	BE786595.1	EST_HUMAN	601478819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'
9935	19404		4.08	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
678	10611	20432	1.68	1.9E-02	AA572764.1	EST_HUMAN	nt19a07.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.H L1 repetitive element;
1599	11504	21364	0.84	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
1993	11887	21779	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1993	11887	21780	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2458	12335	22230	0.87	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2875	12802	22696	7.08	1.9E-02	AA713856.1	EST_HUMAN	nv04f05.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238337 3'
2923	12850	22650	1.53	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3222	13146		0.82	1.9E-02	AB033611.1	NT	Uratrichus talpoides mitochondrial gene for cytochrome b, complete cds
3560	13474		1.25	1.9E-02	N52280.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NkHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3644	13558		5.75	1.9E-02	BE739088.1	EST_HUMAN	601572382F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
							qr04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
3654	13568	23355	0.98	1.9E-02	A301183.1	EST_HUMAN	
3961	13868	23646	1.14	1.9E-02	AF141940.1	NT	Mycoplasma imitans VhaA1 precursor (VhaA1) and VhaA2 precursor (VhaA2) genes, partial cds
4099	13999	23777	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	13999	23778	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
							tf46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4441	14335	24125	2.51	1.9E-02	A452999.1	EST_HUMAN	
4944	12335	22230	1.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 50
5356	15276	25106	1.29	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
6965	16862		1.29	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
7377	17246	27452	1.47	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
7777	17627	27859	1.31	1.9E-02	BF695632.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
9234	19516	25137	2.55	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gillarin mRNA, complete cds
							hm52c06.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
343	10302	20117	1.44	1.8E-02	AW771104.1	EST_HUMAN	MER29 repetitive element;
670	10604	20421	1.14	1.8E-02	BF308122.1	EST_HUMAN	601894323F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1144	11057	20900	1.34	1.8E-02	X17694.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1417	11323	21187	1.23	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2646	12512	22403	1.51	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3174	13099		0.89	1.8E-02	A805829.1	EST_HUMAN	fe52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3812	13724	23513	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3812	13724	23514	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3996	13903		1.15	1.8E-02	AA861446.1	EST_HUMAN	ak24f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4332	14229	24011	1.44	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-307299-071-b11 DT0021 Homo sapiens cDNA
4873	14763	24532	1.05	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
4887	14767	24543	1.06	1.8E-02	A288701.1	EST_HUMAN	qmr06b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881007 3'
6075	16058	26207	3.96	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
							aj62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbl.11672 ZINC FINGER PROTEIN 91 (HUMAN);
7560	17411		2.49	1.8E-02	AA897543.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7790	17640	27873	1.51	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5'
7871	17721	27966	1.23	1.8E-02	XG6933.1	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
8735	17884	28126	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8735	17884	28127	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8886	18697	28991	1.76	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)
8897	18706	29000	3.12	1.8E-02	U82749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rpt2a-3) mRNA, partial cds
9912	19496		1.29	1.8E-02	AF047475.1	NT	Drosophila melanogaster projectin (projectin) gene, partial cds
888	10814	20662	1.29	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1750	11650	21519	2.24	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1750	11650	21520	2.24	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1828	11725		3.08	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2066	11956		13.03	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2603	12471		1.35	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2968	12895	22695	0.92	1.7E-02	A1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3467	13383		4.17	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3573	13487		0.88	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4078	13980		0.98	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4105	14005		1.78	1.7E-02	R02506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124647 5'
4427	14322	24109	1.24	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
4615	14503	24291	1.77	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4708	14594		5.27	1.7E-02	A015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640868 3'
4967	14842	24612	5.47	1.7E-02	AF105037.1	NT	Murid herpesvirus 4 complete genome
5725	16632	25735	1.53	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6276	16140	26296	2.31	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
6554	16412		1.81	1.7E-02	AJ010770.1	NT	Homo sapiens hyperin gene, exons 1-50
7592	17443	27659	1.48	1.7E-02	AL040554.1	EST_HUMAN	DKFZp4340314.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4340314 5'
9781	19683	24995	2.25	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-f08 NN1030 Homo sapiens cDNA
9861	19352		1.96	1.7E-02	Q03211	SWISSPROT	PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
501	10443		1.58	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1635	11539	21399	1.13	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
2202	12089	21990	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	12089	21991	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2518	12392	22284	0.98	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2606	12474	22368	1.47	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2662	12529		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3481	13397	23202	3.83	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-053-C07 CT0219 Homo sapiens cDNA
4084	13986		2.16	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4203	14102	23885	0.94	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-07 PT0012 Homo sapiens cDNA
5456	15377	25437	1.31	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6003	15908	26032	2.11	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6758	16637		4.01	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
7773	17623		2.71	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
7954	17804	28044	1.47	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
7954	17804	28045	1.47	1.6E-02	AA572818.1	EST_HUMAN	P29294 TELOKIN. [1]:
8280	19473	28401	2.17	1.6E-02	Z94828.1	NT	nf19g03.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
8544	18416	28683	2.52	1.6E-02	AL161508.2	NT	P29294 TELOKIN. [1]:
8544	18416	28684	2.52	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LEI0260 (=T1611E11))
8801	18615	28905	1.91	1.6E-02	AI373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
9211	12089	21990	1.35	1.6E-02	Q64176	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
9211	12089	21991	1.35	1.6E-02	Q64176	SWISSPROT	q296610.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
9577	19165		2.3	1.9E-02	X92751.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9773	19433		1.42	1.6E-02	11417966	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
734	10666		24.9	1.9E-02	8923734	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
2095	11984	21879	3.81	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
2128	12016	21914	2.38	1.5E-02	AL161594.2	NT	Homo sapiens transcription factor (HSA130894), mRNA
3023	12951	22743	1.44	1.5E-02	AJ006216.1	NT	y27b07.7 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
3023	12951	22744	1.44	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
						NT	Homo sapiens CACNA1F gene, exons 1 to 48
						NT	Homo sapiens CACNA1F gene, exons 1 to 48

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3663	13577	23365	0.9	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0116-080900-201-b12 TN0115 Homo sapiens cDNA
4049	13951	23727	1.23	1.5E-02	AA160957.1	EST_HUMAN	zq40g10.r1 Stratagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'
4367	14263	24048	0.91	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5901	15707	25819	1.91	1.5E-02	Q09711	SWISSPROT	HYPOPHOSPHATASE 1
6332	16195		1.66	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
6377	16239	26399	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
6596	16476	26664	1.53	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6900	16480	26668	3.44	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
7126	17003	27195	1.23	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bn07 Homo sapiens cDNA clone IMAGE:4154504 5'
7520	17339	27545	2.07	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
7646	17496	27717	1.25	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
7646	17496	27718	1.25	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
8508	18380	28647	2.5	1.5E-02	L40809.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds
9429	19559		1.32	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
9980	19437		1.47	1.5E-02	AU134730.1	EST_HUMAN	AU134730 PLACET1 Homo sapiens cDNA clone PLACET000374 5'
411	10357		1.45	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 94 of the complete genome
1102	11018	20860	3.58	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1236	11143		1.35	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1276	11184		2.82	1.4E-02	U67779.1	NT	Xeropus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1374	11280		0.94	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1501	11405		0.96	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBA-H11 5'
3176	13101	22305	1.9	1.4E-02	AF160959.2	NT	Bifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3352	13272	23074	0.99	1.4E-02	AV074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3439	13356	23161	5.21	1.4E-02	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3439	13356	23162	5.21	1.4E-02	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3476	13392	23197	0.98	1.4E-02	4539328	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3606	13520	23308	6.16	1.4E-02	695918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4387	14283	24062	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4387	14283	24063	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4775	14559	24445	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4775	14559	24446	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5862	15768	25887	4.62	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
5862	15768	25888	4.62	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6732	16612		1.82	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
7408	17275	27481	2.07	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
9128	18885	28790	4.79	1.4E-02	X60459.1	NT	Human FNAR gene for interferon alpha/beta receptor
9476	19102		1.55	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
9753	19277		1.89	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1821	11718		0.86	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1912	11807	21684	2.41	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22906	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3177	13102	22907	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3888	13799		1.41	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5176	11807	21684	1	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5212	15135	24854	1.36	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmxq28orf
5212	15135	24855	1.36	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmxq28orf
6156	15114	24856	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6156	15114	24857	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6473	16332	26499	4.77	1.3E-02	AI031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
6939	16817	27010	1.74	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7862	17712	27956	1.87	1.3E-02	M83707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
8360	18237	28484	4.39	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
8360	18237	28485	4.39	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
9102	19705		2.92	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
9482	19694		1.6	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
9556	19170		1.8	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
9758	19486		28.64	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9949	19744	24912	1.32	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
206	10177		0.94	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
352	10310	20128	1.74	1.2E-02	AA059299.1	EST_HUMAN	z65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element ;
445	10389	20210	1.48	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
721	10853	20483	2.98	1.2E-02	AI183522.1	EST_HUMAN	qd68a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element ;
2130	12018	21916	1.99	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2393	12271	22167	1.23	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2448	12325	22223	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2448	12325	22224	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2866	12271	22167	1.27	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3063	12990		6.18	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3250	13173	22971	1.89	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4830	14712	24495	2.04	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
4874	14849		1.73	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiqT mRNA, partial cds
5017	14891	24659	2.12	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5516	15434	25497	1.96	1.2E-02	D78559.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6180	16066	26216	5.33	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6327	16190	26352	6.37	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
6665	16645	26742	2.11	1.2E-02	Q11205	SWISSPROT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
6765	16644	26832	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
6765	16644	26833	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
7162	17029		1.17	1.2E-02	T76987.1	EST_HUMAN	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
7557	17408	27623	2.45	1.2E-02	AB031013.1	NT	Novwalk-like virus genogroup 2 gene for capsid protein, complete cds
7575	17426	27640	1.23	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
9177	18918	25345	1.78	1.2E-02	OT5534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)
9588	19575		1.5	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
9766	19286		3.47	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557G06 5'
1248	11155	21004	1.32	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1679	11581	21451	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1679	11581	21452	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1992	11886	21778	4.35	1.1E-02	BF345283.1	EST_HUMAN	602018037F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153803 5'
2848	12776		3.53	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285040 5'
2933	12860	22660	10.39	1.1E-02	AF055066.1	NT	Homo sapiens MHC class 1 region
3478	13394	23200	2.46	1.1E-02	AI653508.1	EST_HUMAN	tg95b10.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
3937	13846		0.87	1.1E-02	BE144637.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4016	13921		0.97	1.1E-02	AW813796.1	EST_HUMAN	PM3-HT0175-300999-001-h06 HT0175 Homo sapiens cDNA
4723	14609	24395	1.81	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4821	14704		0.92	1.1E-02	AW820281.1	EST_HUMAN	DKFZp586E0924 s1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586E0924
6480	16339	28506	2.26	1.1E-02	BE149611.1	EST_HUMAN	QV2-S T0296-150200-028-cl1 ST0296 Homo sapiens cDNA
7160	17037	27230	6.87	1.1E-02	Q61982	SWISSPROT	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
							NEUROGENIC LOCUS NOTCH 3 PROTEIN
7710	17660	27785	2.25	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
7810	17660	27900	4.1	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
8347	18224	28476	3.38	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
9064	18845		2.23	1.1E-02	AA668239.1	EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
6	9992	19785	3.35	1.0E-02	AW846120.1	EST_HUMAN	Alu repetitive element
1506	11411	21270	0.81	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2525	12399		1.2	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3051	12978	22771	2.37	1.0E-02	BE835556.1	EST_HUMAN	cc22h08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3226	13150	22950	1.18	1.0E-02	BE968999.1	EST_HUMAN	RC0-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3464	13380		0.99	1.0E-02	AW845621.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933699 3'
3805	13717	23505	0.79	1.0E-02	AI05086.1	EST_HUMAN	MRO-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4667	14553	24345	4.26	1.0E-02	6753521	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4736	14621	24407	2.38	1.0E-02	R96597.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Cnr2), mRNA
4995	14870	24633	0.85	1.0E-02	AF218910.1	NT	yt54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5149	15016		0.82	1.0E-02	BE76539.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced
5751	15659	25766	2.74	1.0E-02	AW577113.1	EST_HUMAN	601486286F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888908 5'
5751	15659	25767	2.74	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6054	16037	26178	2.06	1.0E-02	Z29642.1	NT	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
7403	17270	27475	4.65	1.0E-02	BF036331.1	EST_HUMAN	Z.mays U3snRNA pseudogene
7403	17270	27476	4.65	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8586	18454		2.1	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
8674	18362	28846	2.03	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10.5'
9142	19762		1.7	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
9202	19835	25061	2.95	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
9217	19590		5.22	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
9745	19845		2.44	1.0E-02	X62654.1	NT	H. sapiens gene for Me497/CD63 antigen
875	10801	20651	1.7	9.0E-03	AI796126.1	EST_HUMAN	wh42f09.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1243	11150		1.97	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element;
2346	12226	22123	3.26	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2593	12463	22355	1.08	9.0E-03	AJ243727.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2593	12463	22356	1.08	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12803	22597	0.83	9.0E-03	AI251744.1	EST_HUMAN	(Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12803	22598	0.83	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3617	13531	23317	0.92	9.0E-03	J05184.1	NT	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
4914	14793	24568	1.17	9.0E-03	BE047949.1	EST_HUMAN	S.acidocaldarius thermopsin gene, complete cds
5181	15045		2.56	9.0E-03	AF137240.1	NT	tz44e10.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291466 5'
5997	15902		4.17	9.0E-03	BE745988.1	EST_HUMAN	Sargocentron sp. mixed lineage leukemia-like protein (ML) gene, partial cds
6597	16477		1.18	9.0E-03	AL039991.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7673	17523	27749	1.47	9.0E-03	P20908	SWISSPROT	(DKFZp434L0412_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
8354	18231		1.95	9.0E-03	Y18000.1	NT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
9352	19763		1.34	9.0E-03	BF351141.1	EST_HUMAN	Homo sapiens NF2 gene
9557	19768		11.59	9.0E-03	BE348385.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
9562	15045		1.27	9.0E-03	AF137240.1	NT	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
9649	19215	25259	1.52	9.0E-03	AL163267.2	NT	Sargocentron sp. mixed lineage leukemia-like protein (ML) gene, partial cds
9843	19341		27.64	9.0E-03	BF351141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
493	10436		3.2	8.0E-03	AA723007.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
973	10897	20744	45.2	8.0E-03	AF106656.1	NT	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element;
2113	12002	21900	2.38	8.0E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens chromosome 21 segment HS21C083

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2930	12857		0.86	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mifI), microcin 24 (mtfS), and microcin transport protein (mifA, mifE) genes, complete cds
3270	13191	22990	0.97	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3314	13235	23039	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3792	13704		1.07	8.0E-03	AF058764.1	NT	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
4286	14185	23966	5.12	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5391	15310	25164	2.7	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5761	19453	25775	1.35	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6048	15951	26081	4.52	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6279	16143	26299	2.19	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
6453	16314		1.86	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7166	17043	27235	3.81	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
7717	17567		4.72	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
8148	18036	28284	1.92	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
8353	18230		2.78	8.0E-03	Z49652.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
8687	18575	28858	1.75	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8687	18575	28859	1.75	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8953	18760	29053	4.83	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
9075	18852		1.34	8.0E-03	M65035.1	NT	Oryctolagus cuniculus elf-2a kinase mRNA, complete cds
9121	18882		3.36	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
679	10612	20433	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20434	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
961	10884	20732	2.01	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1100	11016	20858	2.6	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZE10 5'
1341	11247		1.19	7.0E-03	Q51060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1373	11279	21135	13.73	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HIF-2)
1486	11391	21251	4.6	7.0E-03	AW303599.1	EST_HUMAN	ab79b09.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2210	12715	22001	2.24	7.0E-03	P04929	SWISSPROT	xx21b02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3702	13616	23400	1.27	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
							UI-H-B13-akb-c-10-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3741	13653	23436	1.01	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4434	14329		1.23	7.0E-03	AW117711.1	EST_HUMAN	xe34f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987
4495	14389		1.01	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN.;
4916	14795		1.76	7.0E-03	AL163278.2	NT	hh89a05.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869636 5'
							Homo sapiens chromosome 21 segment HS21C078
5038	14910	24683	1.1	7.0E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:Q93434
5038	14910	24684	1.1	7.0E-03	BE044191.1	EST_HUMAN	Q93434 RETICULOCALBIN.;
5717	19452		5.07	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
5813	15718	25831	1.49	7.0E-03	W68251.1	EST_HUMAN	zd33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
5939	15844	25967	3.46	7.0E-03	AA327129.1	EST_HUMAN	EST30674 Colon I Homo sapiens cDNA 5' end
5954	15859	25980	1.3	7.0E-03	BE857385.1	EST_HUMAN	7g34b10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6210	16592	26127	2.39	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2 ; contains TAR1.42 TAR1 repetitive element;
6441	16302	26466	4.98	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
6441	16302	26467	4.98	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
6723	16603	26792	2.29	7.0E-03	BE175667.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBL077w
7605	17456	27670	2.53	7.0E-03	P48982	SWISSPROT	RQ5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
7605	17456	27671	2.53	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7906	17756		1.27	7.0E-03	AV687378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8201	18086	28337	3.36	7.0E-03	AB008852.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAF007 5'
							Bos taurus mRNA for NDP52, complete cds
							Yr15h01.s1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
9609	19750		1.55	7.0E-03	H94065.1	EST_HUMAN	Alu repetitive element;
9615	19194		1.88	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
9962	19425		1.83	7.0E-03	AW868110.1	EST_HUMAN	RQ0-SN0052-110400-021-e04 SN0052 Homo sapiens cDNA
1220	11129	20979	9.29	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
1220	11129	20980	9.29	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2744	12606	22499	1.09	6.0E-03	AF112374.1	NT	SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2862	12790	22581	3.11	6.0E-03	AA759135.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
2862	12790	22582	3.11	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3208	13132		2.06	6.0E-03	H75690.1	EST_HUMAN	yr7h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3264	13187		0.82	6.0E-03	AF190338.1	NT	Nctoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13256	23092	1.24	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3336	13256	23063	1.24	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3499	13416		1.05	6.0E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3610	13524	23311	3.62	6.0E-03	BF510986.1	EST_HUMAN	UIH-B14-apm-c-08-0-JL.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3711	13624	23407	1.28	6.0E-03	6754023	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp1), mRNA
3846	13757	23551	0.93	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240699-021-b10 CT0204 Homo sapiens cDNA
3873	13784		1.18	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4231	14129		0.87	6.0E-03	N58946.1	EST_HUMAN	ya62h10.s1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'
4267	14166		1.37	6.0E-03	AI016833.1	EST_HUMAN	ov83c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4597	14485	24271	6.82	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5115	14983	24758	1.83	6.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5129	14996	24767	0.89	6.0E-03	AA889972.1	EST_HUMAN	aj95g09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
5506	16365	26542	1.97	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
5586	16466	26657	7.04	6.0E-03	AI033980.1	EST_HUMAN	ov13a04.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
5650	16530	26724	2.44	6.0E-03	AW799337.1	EST_HUMAN	RC0-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA
6689	16569		1.41	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
7509	17297	27506	8.21	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7776	17626		1.94	6.0E-03	AI432861.1	EST_HUMAN	ti22c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
7949	17799	28039	1.5	6.0E-03	X68386.1	NT	M.thermoformicum complete plasmid pFV1 DNA
8127	18015	28263	2.23	6.0E-03	AW9662164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
8186	18072		2.21	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
8220	18102	28356	1.89	6.0E-03	AI420786.1	EST_HUMAN	te91c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.;
8220	18102	28357	1.89	6.0E-03	AI420786.1	EST_HUMAN	te91c12.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.;
8350	18227		3.91	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
8351	18228	28479	3.54	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9185	18922		1.59	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450290 (section 39 of 148) of the complete genome
9372	19038		1.34	6.0E-03	AB025356.1	NT	Anguilla japonica mRNA for activin B, complete cds
9392	19583		2.21	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9722	19262		1.57	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
9741	19274		1.34	6.0E-03	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
653	10589	20406	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
653	10589	20407	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20406	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20407	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1096	11012	20854	1.38	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1552	11457		0.91	5.0E-03	A1138977.1	EST_HUMAN	qp79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2648	12515	22405	3.44	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2905	12832	22629	0.95	5.0E-03	BE268057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3097	13024	22820	4.08	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3116	13041		1.75	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3129	13054	22853	1.04	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2N4HBst Homo sapiens cDNA clone IMAGE:155666 3'
3240	13163		1.08	5.0E-03	AJ297367.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3641	13555	23341	4.16	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3698	13612	23396	0.83	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3890	13801		1.38	5.0E-03	AA2399675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4207	14106	23886	0.93	5.0E-03	H78355.1	EST_HUMAN	Yr79g10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240066 5'
4209	13612	23396	0.91	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4503	14396	24181	0.94	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4619	14507	24296	2.49	5.0E-03	A1752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random
5541	15458	25528	5.34	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5685	15594	25895	2.43	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLSTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5977	15881		6.17	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6091	15101	24877	6.02	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6566	16424	26605	6.26	5.0E-03	AB016816.1	NT	Homo sapiens MAS1.1 mRNA, complete cds
6794	16673	26865	1.97	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7006	16883		6.92	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8103	17993		7.44	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
8310	18187	28435	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2 L1 repetitive element;
8310	18187	28436	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2 L1 repetitive element;
8399	18275	28527	1.95	5.0E-03	T49153.1	EST_HUMAN	y039e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
8433	18307	28563	1.77	5.0E-03	10945753	NT	Mus musculus hypothetical protein, MNCB-4760 (LOC58212), mRNA
8644	19308		3.73	5.0E-03	BE048055.1	EST_HUMAN	tz46e04.y1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
9327	19709		5.04	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
9460	19091		8.65	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
9555	19153		1.55	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
9592	19174		1.28	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT;
9916	19529		4.16	5.0E-03	BF572332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9791	19301	25197	1.94	5.0E-03	AW449109.1	EST_HUMAN	U1H-B13-akt-f08-0-J1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
9808	19601		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA (VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
9929	19400		1.41	5.0E-03	AI668709.1	EST_HUMAN	zb74g05.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309368 3'
232	10201	20015	2.97	4.0E-03	AW500196.1	EST_HUMAN	U1HF-BN0-akt-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
318	10280	20097	2.18	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
436	10380	20203	0.94	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (P13K)
588	10526	20333	3	4.0E-03	AA939330.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562563 3'
859	10785	20637	1.81	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
893	10819		3.43	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1133	11047	20869	32.55	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1153	11066	20910	1.58	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1281	11189	21040	1.33	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.t1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1598	11472		1.31	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1709	11610	21480	2.2	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
1971	11864	21757	20.87	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:510398 5'
2200	12087		1.66	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2232	12117	22019	1.46	4.0E-03	AW794740.1	EST_HUMAN	RC6-JUN0014-170400-023-G01 UN0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2526	12400	22290	1.89	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
							Homo sapiens polyglutamine-containing C14ORF4 gene
2526	12400	22291	1.89	4.0E-03	U52111.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2659	12526	22414	2.86	4.0E-03	AJ277395.1	NT	Homo sapiens chromosome 21 segment HS21C084
2659	12526	22415	2.86	4.0E-03	AJ277395.1	NT	Homo sapiens chromosome 21 segment HS21C084
2664	12530	22418	1.02	4.0E-03	AL163284.2	NT	x98f04.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2666279 3'
3487	13403	23207	0.94	4.0E-03	AW188426.1	EST_HUMAN	x98f04.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2666279 3'
3487	13403	23208	0.94	4.0E-03	AW188426.1	EST_HUMAN	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3572	13486	23278	0.8	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3836	13486	23278	0.83	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3852	13763	23556	0.85	4.0E-03	AF060888.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3914	13823		1.79	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
							ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4509	14402	24190	1.13	4.0E-03	AJ732754.1	EST_HUMAN	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
5164	15030	24796	13.17	4.0E-03	J02187.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5225	15149	24916	1.66	4.0E-03	AF005859.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5315	15236	25039	19.53	4.0E-03	AF169825.1	NT	(HPRC)
5540	15457	25527	4.23	4.0E-03	P04196	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
5542	15459	25529	1.5	4.0E-03	P21849	SWISSPROT	Rattus norvegicus opsin gene, complete cds
5704	15612		3.23	4.0E-03	U22180.1	NT	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461964 5'
5809	15714	25827	1.76	4.0E-03	BE548453.1	EST_HUMAN	Lyoparsicon esculentum knotted 3 protein (TKn3) mRNA, complete cds
6062	16045	26190	1.52	4.0E-03	U76408.1	NT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6271	16136	26291	4.14	4.0E-03	Q02817	SWISSPROT	Dictyostellium discoideum A44 development protein DG1122 (DG1122) gene, partial cds
6690	16570	26762	3.61	4.0E-03	AF111944.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6774	16653	26841	2.02	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7066	16933	27123	7.4	4.0E-03	AI553983.1	EST_HUMAN	U49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
7151	17028		4.41	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7159	17036	27229	3.38	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8472	18345	28609	5.64	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9295	19725		3.95	4.0E-03	BE15173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
9317	19009		2.25	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
9628	19202		3	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element ;
9666	19640		1.57	4.0E-03	AW614596.1	EST_HUMAN	HH02007.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element
9679	19236		1.57	4.0E-03	AW819141.1	EST_HUMAN	LTR5 repetitive element ;
9950	19416	25168	1.52	4.0E-03	11436955	NT	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
367	10323	20146	1.62	3.0E-03	AF011920.1	NT	Homo sapiens Grib2-associated binder 2 (KIAA0371), mRNA
861	10787	20638	7.66	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1638	11542	21401	1.84	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2211	12097		0.87	3.0E-03	AF055066.1	NT	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2248	12132		3.9	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2249	12133	22029	1.12	3.0E-03	U46858.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2249	12133	22030	1.12	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2963	12890		0.84	3.0E-03	Y09006.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3044	12971	22765	4.53	3.0E-03	BE379296.1	EST_HUMAN	Arabidopsis thaliana rpm1 gene
3112	13037	22833	2.62	3.0E-03	AW802687.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3371	13290	23089	1.95	3.0E-03	U34606.1	NT	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3379	13297		6.75	3.0E-03	Y12500.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3895	13805	23591	7.43	3.0E-03	AV762392.1	EST_HUMAN	C.elegans samc gene
3895	13805	23592	7.43	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3950	13858	23632	1.58	3.0E-03	AI792278.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4058	13960		1.34	3.0E-03	Z32521.1	NT	af04f09.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4296	14194	23978	11.91	3.0E-03	AJ011432.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4417	14311	24096	4.37	3.0E-03	AI536141.1	EST_HUMAN	Rattus norvegicus gdnf gene
4630	14518	24309	0.88	3.0E-03	AL119087.1	EST_HUMAN	xl8.P10.H3 conorm Homo sapiens cDNA 3'
							DKFZp761B0712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	14913	24399	1.54	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4745	14630	24416	7.09	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5089	14959	24733	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5089	14959	24734	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5220	15143	24837	3.17	3.0E-03	8922489	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5410	15330	25380	1.41	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5946	16851	25974	9.97	3.0E-03	AA456701.1	EST_HUMAN	aa13f10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6277	16141	26297	1.54	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcp3 gene for putine-cytosine permease
6442	16303	26468	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bz1P protein, complete cds
6741	16620	26809	2.01	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:304783 3'
6928	16806	27001	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
6940	16818	27011	1.57	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6991	16868		1.38	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
7199	17076		8.52	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCL_CGAP_GLU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.11 L1 repetitive element;
7230	17107	27297	4.1	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
7244	17121	27317	8.9	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_mel1 HISTONE H2B.2 (HUMAN);
7598	17449		3.48	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
7694	17544	27768	1.29	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
7742	17592	27813	1.46	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
7836	17686	27931	4.05	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8222	18104		2.69	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (H-EB), mRNA
8685	18573	28856	2.11	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
8744	18593	28137	2.01	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
8773	18590	28877	3.06	3.0E-03	AF094481.1	NT	Homo sapiens triniticotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8773	18590	28878	3.06	3.0E-03	AF094481.1	NT	Homo sapiens triniticotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8841	18654	28942	1.93	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9068	19542		2.02	3.0E-03	AI525056.1	EST_HUMAN	promina-5.E07.1 bvtumor Homo sapiens cDNA 5'
9103	19870	28780	1.54	3.0E-03	AA983154.1	EST_HUMAN	α77b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	19668		1.35	3.0E-03	AB009868.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
9339	19019	25296	2.33	3.0E-03	AJ206282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
504	10446	20258	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
504	10446	20259	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	12677		7.01	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1340	11246	21104	1.93	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1343	11249	21106	1.59	2.0E-03	AA681605.1	EST_HUMAN	nu86f01.s1 NCL CGAP_A17 Homo sapiens cDNA clone IMAGE:1217593
1353	11259	21115	12.6	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1474	11379	21243	1.11	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1500	11404	21263	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1500	11404	21264	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1573	11477		4.94	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1733	11634	21502	1.38	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares fetal_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1950	11846	21731	2.17	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2203	12090	21992	1.04	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2535	12409		4.62	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-0-UI.st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3370	13289	23088	4.03	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares fetal_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3376	13294	23093	1.02	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3615	13529	23315	4.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
3869	13780	23572	0.92	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4024	13927	23703	2.15	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEINCONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4127	14027		9.77	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4446	14340	24130	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4446	14340	24131	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4608	14496	24285	0.94	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4612	14500		1.7	2.0E-03	R87773.1	EST_HUMAN	y445e02.st Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5077	14947		0.82	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
5194	15057	24820	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
5194	15057	24821	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5372	15292	25128	1.37	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5457	19445	25438	1.76	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5501	15420	25482	1.87	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
5716	15624	25725	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5716	15624	25726	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5829	15735	25846	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5829	15735	25847	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5831	15737	25848	7.14	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5850	15756	25874	2.2	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5961	15767	25886	1.95	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
5979	15884		1.36	2.0E-03	A1891089.1	EST_HUMAN	wu36h09.x1 Soares Disgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:R129 HUMAN P47914 90S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element ;
6212	15994	26129	2.88	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0366-061269-054-401 BT0366 Homo sapiens cDNA
6691	16671	26763	2.11	2.0E-03	AW592004.1	EST_HUMAN	h837b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2634035 3' similar to TR:Q60976 Q60976 JERKY ;
6784	16663	26853	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
6784	16663	26854	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
7513	17301	27508	3.12	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
7775	17625		5.41	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
8379	18256		2.78	2.0E-03	M86524.1	NT	Human dystrophin gene
8779	18350	26520	1.78	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8829	18642		1.77	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
8836	18649	28936	12.17	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
9052	18835		2.07	2.0E-03	A1625745.1	EST_HUMAN	t95h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
9066	18847	29115	2.88	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
9113	14947		4.48	2.0E-03	AJ245187.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
9322	19703		2.76	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKOGXD05 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	19066	25278	1.59	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
9455	19087		9.62	2.0E-03	D84278.1	NT	Human DNA for CD38, exon 1
9525	19134		2.92	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9582	19569		1.57	2.0E-03	AI375037.1	EST_HUMAN	ta69f02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;
9696	19247		1.27	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9656	19521		1.66	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
432	10377	20198	1.38	1.0E-03	H96471.1	EST_HUMAN	y98c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
812	10740	20587	2.38	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
812	10740	20598	2.38	1.0E-03	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1079	10995	20836	2.14	1.0E-03	AI865788.1	EST_HUMAN	as70b08.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1099	11015	20857	1.44	1.0E-03	AI854572.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1150	11063	20906	1.45	1.0E-03	AI692816.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422289 3'
1982	11875	21768	3.61	1.0E-03	PA7808	SWISSPROT	wk86a06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2108	11997	21896	8.02	1.0E-03	AI131016.1	NT	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2951	12878	22676	1.15	1.0E-03	AB033117.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMMI)
3154	13079	22879	2.26	1.0E-03	P18915	SWISSPROT	Homo sapiens SCL gene locus
3154	13079	22880	2.26	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3262	13185	22984	1.16	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3496	13413	23218	0.79	1.0E-03	U68061.1	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3496	13413	23219	0.79	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3614	13528		1.24	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3855	13763	23559	1.02	1.0E-03	Z49649.1	NT	Human MUC2 gene, promoter region
4334	14231	24013	3.54	1.0E-03	BE939162.1	EST_HUMAN	Human MUC2 gene, promoter region
4377	14273	24054	3.77	1.0E-03	BE246336.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4564	14456	24244	0.87	1.0E-03	U29449.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
							RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
							TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
							Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	14603	24388	1.78	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4717	14603	24389	1.78	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4718	14604		6.23	1.0E-03	BE154087.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5009	14883	24649	16.98	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5103	14971	24747	0.93	1.0E-03	AV685870.1	EST_HUMAN	AV685870 GK Homo sapiens cDNA clone GKCDME11 5'
5250	15173	24946	2.03	1.0E-03	AA200951.1	EST_HUMAN	zs44f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	15238	25042	3.06	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5349	15269	25096	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5349	15269	25097	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5423	15344	25397	1.69	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5686	15577		4.08	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5788	15668		8.56	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
5824	15730	25842	1.32	1.0E-03	T87761.1	EST_HUMAN	yd93at1.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:115772 5'
5857	15763		1.4	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6242	16108	26259	2.4	1.0E-03	D18826.1	NT	Human gene for fourth somatostatin receptor subtype
6419	16281		1.37	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
6503	16362	26537	1.63	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6536	16394	26573	3.13	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1, 2 and 3
6636	16516	26707	5.35	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6798	16677	26867	2.39	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
7175	17052		1.4	1.0E-03	Y11204.1	NT	V.carteri gene encoding valvovopsin
7273	17150	27345	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7273	17150	27346	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7541	17392	27602	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
7541	17392	27603	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
8056	17947	28196	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8056	17947	28197	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8133	18021	28268	2.44	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
8198	18083		2.69	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195
8497	18370		3.4	1.0E-03	AI759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
9046	18831	29113	2.82	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9491	19108	25287	1.95	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
9517	19887		2.15	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
9626	19707	24904	4.2	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5131	14998	24769	0.81	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5485	15404		1.56	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
7561	17412		1.42	9.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgbAS1 mRNA for beta-amylin synthase, complete cds
1472	11377		1.39	8.0E-04	X96469.1	NT	X.laevi mRNA for C4SR protein
3843	13754	23548	1.27	8.0E-04	R07008.1	EST_HUMAN	yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
4089	13989		4.2	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4656	14542	24332	2.39	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
8485	18358		2.08	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares fetal heart NbH19W Homo sapiens cDNA clone IMAGE:377874 3'
8616	18483		2.16	8.0E-04	AI577099.1	EST_HUMAN	tn85a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1766	11684	21562	1.51	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2350	12230	22127	1.13	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2682	12547	22437	3.26	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3243	13166	22965	1.03	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
5923	15828		2.24	7.0E-04	AI769331.1	EST_HUMAN	w936f09.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
8851	18663		3.2	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8871	18683	28973	2.61	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
9558	19155		3.29	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
9780	19300		2.72	7.0E-04	R17336.1	EST_HUMAN	y913c06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
9813	19321		3.28	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPE-1), mRNA
3877	13788	23576	1.34	6.0E-04	AI862525.1	EST_HUMAN	wf15a11.x1 NCL_CGAP_K12 Homo sapiens cDNA clone IMAGE:2402876 3'
3999	13905	23680	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region
3999	13905	23681	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGH-EP1) gene, 5' flanking region
4092	13992	23769	3.28	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6590	18470		4.35	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7733	17883		3.13	6.0E-04	AL048507.2	EST_HUMAN	DKFZp568M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp568M2024
7800	17650	27887	2.24	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
8776	18593	28881	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8852	18664	28950	6.32	6.0E-04	AW013847.1	EST_HUMAN	UH-H10-aab-e-09-UJ1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
8906	18714		2.45	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NM23-M2) (P18)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9225	19598		2.26	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
9958	19421	25170	1.49	6.0E-04	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
635	10572	20385	5.82	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF62)
1485	11390		1.83	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3367	13286	23085	1.42	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCL_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
5381	15281	25113	2.19	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5996	15901	26026	5.72	5.0E-04	AA155080.1	EST_HUMAN	zo33508.r1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
6364	16227	26387	13.5	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
6639	16519	26710	5.57	5.0E-04	AI188382.1	EST_HUMAN	gd13f06.x1 Soares_placenta_8to8weeks_2NBH-P8b9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X57602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
7345	17213	27412	1.45	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
7543	17394	27606	4.69	5.0E-04	AW270938.1	EST_HUMAN	xs06e02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
8343	18220		4.17	5.0E-04	AL048507.2	EST_HUMAN	DKFZp566M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp566M2024
8950	15281	25113	17.6	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9164	19530		2.27	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
9944	19413		1.46	5.0E-04	AW241666.1	EST_HUMAN	xm77h09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2690273 3'
386	10333		1.13	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
657	10592	20410	1.42	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 83 of 163 of the complete genome
829	10756	20606	1.57	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
829	10756	20607	1.57	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE ;
1449	11354	21218	3.92	4.0E-04	AW753356.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE ;
2037	11928	21823	1.68	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-101 CT0254 Homo sapiens cDNA
2086	11976		1.19	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2586	12457	22348	2.73	4.0E-04	O96615	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3127	13052	22850	1.89	4.0E-04	AF281074.1	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3316	13237	23041	0.84	4.0E-04	AV696624.1	EST_HUMAN	Homo sapiens neuropln 2 (NRP2) gene, complete cds, alternatively spliced
4228	14126	23900	2.75	4.0E-04	AA576331.1	EST_HUMAN	AV696624 GK Homo sapiens cDNA clone GKOFFH07 5'
							nh10a10.s1 NCL_CGAP_Co11 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	14126	23901	2.75	4.0E-04	AA576331.1	EST_HUMAN	rh10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4437	14332	24121	1.28	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5020	14893	24661	3.72	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5132	14999	24770	0.9	4.0E-04	N48313.1	EST_HUMAN	y78b10.s1 Soares multiple sclerosis_2N6HMSF Homo sapiens cDNA clone IMAGE:279643 3' similar to contains Alu repetitive element;
6972	16849	27040	1.62	4.0E-04	N25507.1	EST_HUMAN	y39e12.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:264142 5'
7588	17439	27655	2.79	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1944341 3'
7662	17512		1.44	4.0E-04	AF022855.1	NT	Mus musculus neurexophilin-2(a17) mRNA, alternatively spliced, complete cds
9526	19505		1.52	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
9677	19479		1.84	4.0E-04	Q05860	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)
150	10124	19942	3.04	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: haryn2) Homo sapiens cDNA clone DKFZp761J221 5'
188	10160	19977	2.22	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
862	10788	20539	1.27	3.0E-04	U93991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1810	11707		1.16	3.0E-04	AI369874.1	EST_HUMAN	th23a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2116082 3'
3268	13190	22988	3.37	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3882	13793	23581	3.63	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3969	13876		1.18	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4711	14597		4.5	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4784	14669	24456	0.85	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
5052	14924		1.34	3.0E-04	Y11204.1	NT	V.cartel gene encoding volvoxopsin
5735	15643		4.82	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6081	16026	26166	5.88	3.0E-04	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
6806	16885	26875	3.49	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
7705	17555	27780	1.42	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
7977	17827	28068	3.66	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
9118	19726	24908	2.33	3.0E-04	AA228301.1	EST_HUMAN	nc38e04.r1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element ;
9483	19576	25068	4.32	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
9874	19361		2.01	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547L185 5'
169	10141	19957	1.18	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
470	10413	20232	2.15	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
889	10815	20663	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
889	10815	20664	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
1162	11075		4	2.0E-04	AI286021.1	EST_HUMAN	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element:
1169	11081		1.99	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1791	11689		1.44	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
2136	12024		1.29	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element:
2528	12402	22293	4.15	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
2958	12885	22683	1	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3'
3389	13307	23105	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0038-070500-194-b07 BT0636 Homo sapiens cDNA
3417	13334	23138	0.98	2.0E-04	U34374.1	NT	Human tyrosine kinase TXK (tkk) gene, exons 9 and 10
3837	13748	23541	0.78	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4051	13953		4.81	2.0E-04	U01029.1	NT	Phaeosolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4569	14461	24249	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4569	14461	24250	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4689	14575		1.31	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4991	14866	24630	1.7	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5403	15322	25371	1.63	2.0E-04	AY654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5411	15331	25381	1.68	2.0E-04	AI690862.1	EST_HUMAN	tc03b11.x1 NCL_OGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
6291	16155		2.5	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
6493	16352		11.07	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6497	16356	26527	1.6	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
6638	16518	26708	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6638	16518	26709	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6819	16698	26890	1.19	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6819	16698	26891	1.19	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6982	16859	27054	2.29	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7729	17579	27801	1.46	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
7754	17604	27828	1.71	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
8225	18107	28360	6.14	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
8515	18387		1.88	2.0E-04	AI243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8625	18490	28762	5.57	2.0E-04	AI440282.1	EST_HUMAN	U01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
8726	18582	28866	2.94	2.0E-04	AW138740.1	EST_HUMAN	UI-H-B1f-adm-c-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
750	10680	20516	0.98	1.0E-04	H98646.1	EST_HUMAN	yv26c09.s1 Scores melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element;
1059	10976	20819	2.43	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1098	11014	20855	3.87	1.0E-04	AW013847.1	EST_HUMAN	ENDONUCLEASE]
1098	11014	20856	3.87	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1310	11216		2.97	1.0E-04	U62918.1	NT	UI-H-B10-aab-e-09-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
							Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1610	11515	21374	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1610	11515	21375	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1817	11714	21594	1.67	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2600	12469	22363	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2600	12469	22364	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2655	12622	22411	1.15	1.0E-04	BE218833.1	EST_HUMAN	hva45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2655	12622	22412	1.15	1.0E-04	BE218833.1	EST_HUMAN	hva45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3247	13170	22969	1.04	1.0E-04	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3675	13589	23376	1.1	1.0E-04	AI440282.1	EST_HUMAN	U01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
3971	13878	23654	1.78	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
3991	13898	23675	1.08	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
4362	14258	24043	0.85	1.0E-04	P09547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5028	14901	24671	1.56	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit: BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5028	14901	24672	1.56	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5033	14905	24676	0.99	1.0E-04	A1357156.1	EST_HUMAN	qx62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
5148	15015		0.9	1.0E-04	Z72560.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL038c
5572	15487	25563	1.36	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6264	16129	26283	12.77	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985583 3'
6468	16129	26283	14.47	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985583 3'
7380	17249	27455	2.53	1.0E-04	AB06220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
7384	17263	27458	1.46	1.0E-04	Q88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGONIC PROTEIN PRECURSOR (CYSTATIN 8)
7562	17413	27628	1.75	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
7848	17698		3	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8649	18513		2.17	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8913	18721	28012	1.98	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
9035	18824		1.84	1.0E-04	BE696769.1	EST_HUMAN	CM0-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA
9566	19158		1.65	1.0E-04	AW893325.1	EST_HUMAN	CM2-NN0010-220300-124-d08 NN0010 Homo sapiens cDNA
983	10616	20439	1.7	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
3995	13902	23678	0.8	9.0E-05	A1762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MIER6.t1 MIER6 repetitive element;
5528	15543	25632	1.47	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7455	17264		2.9	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
7457	17266	27470	2.93	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
8479	18352	28617	2.6	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
8568	18436	28705	1.85	9.0E-05	A1287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
8890	15543	25632	4.4	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
9329	19608		4.17	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
804	10733	20576	1.46	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
846	10773		3.53	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2920	12847		0.78	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4852	15080		1.16	8.0E-05	F28172.1	EST_HUMAN	HSPD16734 HM3 Homo sapiens cDNA clone s3000003H04
8491	18364	28630	1.87	8.0E-05	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9911	19589		3.45	8.0E-05	AA279333.1	EST_HUMAN	z88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
344	10303	20118	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
344	10303	20119	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
555	10496	20302	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
555	10496	20303	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1039	10957	20800	2.32	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2886	12551	22440	5.24	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3121	13046	22843	5.78	7.0E-05	AB009080.1	NT	Dicystellum discoidium gene for TRFA, complete cds
4276	14175	23853	1.27	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4344	14241	24023	0.82	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
4842	14723	24506	0.84	7.0E-05	9845300	NT	Rat cytomegalovirus Maestricht, complete genome
5202	15065		1.12	7.0E-05	AA367612.1	EST_HUMAN	EST78713 Placenta I Homo sapiens cDNA
7508	17296	27505	3.04	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
8501	18374		2.89	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
1981	11874	21766	1.57	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1981	11874	21767	1.57	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2544	12418	22309	1.42	6.0E-05	AI655241.1	EST_HUMAN	wb54h06.x1 NCI_CGAP_GCB6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN).
2652	12519	22409	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2652	12519	22410	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2783	10598	20415	2.45	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5605	15519	25599	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5605	15519	25600	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5855	15761	25879	1.49	6.0E-05	NT2829.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:246212 5'
6918	16796	25983	2.61	6.0E-05	AW856629.1	EST_HUMAN	PM4-NN0080-310300-001-f10 NN0050 Homo sapiens cDNA
7330	17234	27437	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7330	17234	27438	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7484	17354	27558	1.28	6.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
8131	18019	28267	3.88	6.0E-05	R75639.1	EST_HUMAN	y69d08.s1 Soares placenta Nib2HP Homo sapiens cDNA clone IMAGE:119062 5'
8807	18621	28911	3.59	6.0E-05	AA044015.1	EST_HUMAN	repetitive element; contains LTR7 repetitive element ;
9534	19587	25073	8.44	6.0E-05	AW890110.1	EST_HUMAN	2k59f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
							MRO-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit: BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	19427		1.54	6.0E-05	BE58403.1	EST_HUMAN	7g28a08.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3307766 3'
1382	11287	21141	14.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1819	11716		1.63	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55896), mRNA
2831	12760	22550	0.88	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
3897	13807	23593	2.99	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5392	15311	25165	9.01	5.0E-05	X88855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
5646	15559	25652	3.46	5.0E-05	AY653544.1	EST_HUMAN	AY653544 GIC Homo sapiens cDNA clone GLODMA06 3'
9326	19173		2.96	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
9590	19173		3.47	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2776	10193		4.58	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
7486	17356		7.17	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
8150	18038	28286	4.6	4.0E-05	AW627946.1	EST_HUMAN	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;
9287	18989		2.17	4.0E-05	AW117590.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
665	10599	20417	0.84	3.0E-05	AJ248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1043	10991	20804	1.36	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1115	11030	20870	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1115	11030	20871	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
2888	12553	22442	0.91	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4285	14184	23964	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4285	14184	23965	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4365	14281	24045	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4365	14281	24046	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4519	14412	24197	0.85	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4731	10599	20417	0.84	3.0E-05	AJ248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
5151	15018	24786	0.97	3.0E-05	AV726630.1	EST_HUMAN	AV726630 HTC Homo sapiens cDNA clone HTCCEA01 5'
5412	15332	25382	1.54	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myk2p), mRNA
6611	16491	26677	2.23	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
6863	16742	26935	1.62	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
7154	17031	27225	1.65	3.0E-05	AW770382.1	EST_HUMAN	h194e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
7158	17035	27228	1.5	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
7373	17242	27447	1.33	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	17421		3.15	3.0E-05	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
2276	12160	22058	1.76	2.0E-05	A1286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2538	12412	22302	3.02	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element ; Human adenosine deaminase (ADA) gene, complete cds
2681	12546		7.21	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
3098	13025	22821	1.5	2.0E-05	BE06036.1	EST_HUMAN	contains Alu repetitive element; contains element L1 repetitive element ;
3304	13225	23027	0.94	2.0E-05	AF184614.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3323	13243	23050	1.14	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3449	13366		1	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3737	13649		0.85	2.0E-05	AL039107.1	EST_HUMAN	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4510	14403	24191	0.99	2.0E-05	A1263349.1	EST_HUMAN	DKFZp5681064_r1 566 (synonym: ltkd2) Homo sapiens cDNA clone DKFZp5681064 5'
4592	14480		1.06	2.0E-05	BE378471.1	EST_HUMAN	q113a08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1932374 3' similar to contains
4782	14666	24453	0.81	2.0E-05	AJ131016.1	NT	MER18.b3 MER18 repetitive element ;
5520	15438	25602	1.42	2.0E-05	AJ011712.1	NT	Homo sapiens SCL gene locus
5993	15896	26022	2.19	2.0E-05	AA714330.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	15972	26108	2.19	2.0E-05	Y08926.1	NT	rw06d12.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6136	15983		8.04	2.0E-05	A991025.1	EST_HUMAN	P.falcipterus mRNA for AARPI protein, partial
							wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6243	16109	26260	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6243	16109	26261	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6603	16483	26671	2.3	2.0E-05	A381040.1	EST_HUMAN	tg20h05.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
8024	17874	28116	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHF8to9W Homo sapiens cDNA clone IMAGE:259570 5'
8024	17874	28117	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHF8to9W Homo sapiens cDNA clone IMAGE:259570 5'
8039	15983		2.42	2.0E-05	A1991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
8748	17897	28141	2.93	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
9335	19514		2.98	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2 ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9442	19677		3.73	2.0E-05	AW074604.1	EST_HUMAN	xa89a03.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2673932 3' similar to contains L1.b3 L1 repetitive element;
9486	19503		2.25	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9637	19208	26257	1.81	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2663	12729	22417	1.81	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3569	13513	23301	1.67	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3886	13797	23583	9.24	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4082	13984	23761	1.09	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4180	14080	23853	2.01	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4742	14627	24413	2.15	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
4882	14763	24539	4.46	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6049	15952	26082	1.42	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
6211	15993	26128	3.54	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 repetitive element;
6213	16079	26228	6.45	1.0E-05	4508844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6572	16430		1.8	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7168	17045		2.18	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7240	17117	27312	2.48	1.0E-05	AA452578.1	EST_HUMAN	z35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
7352	17220	27420	11.8	1.0E-05	AA238110.1	EST_HUMAN	zs05e11.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
7704	17554	27778	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-aggk-a-08-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7704	17554	27779	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-aggk-a-08-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7851	17701		1.78	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
8291	18170	28414	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
8291	18170	28415	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
2837	12504	22398	6.59	9.0E-06	AI583811.1	EST_HUMAN	ht73a06.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3057	12984	22776	3.66	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2Nbl-P8to9w Homo sapiens cDNA clone IMAGE:1759191 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3559	13473		2.94	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5599	15513	25591	2.58	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6570	16428	26611	10.24	9.0E-06	A1034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
6931	16809	27004	1.16	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7192	17069	27257	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7192	17069	27258	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7317	17193	27394	4.58	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
8309	18196	28434	3.35	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2483	12722	22251	1.55	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-111 CT0283 Homo sapiens cDNA
8992	18796	29087	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
8992	18796	29088	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
963	10896		1.7	7.0E-06	AA699729.1	EST_HUMAN	ab00f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ;
1420	11326	21191	3.19	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2844	12772		6.66	7.0E-06	A1368252.1	EST_HUMAN	qw16g09.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3516	13432		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5493	15412		5.73	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
9072	19698	24900	5.39	7.0E-06	BF215972.1	EST_HUMAN	601881622FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2887	12814	22607	1.09	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3635	13549	23336	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4647	12838	22637	1.77	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4663	14539	24328	2.01	6.0E-06	A1040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ;
5281	15203	24979	1.46	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
7670	17520		1.88	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
9900	19377	25195	1.8	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5695	15604	25706	3.58	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5825	15731	25843	1.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7817	17667	27907	6.9	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9795	19311	25204	4.74	5.0E-06	A065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
631	10568	20380	4.41	4.0E-06	R16287.1	EST_HUMAN	ya48c03.r1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
828	10755	20605	9.3	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1312	11218	21074	5.18	4.0E-06	A1334928.1	EST_HUMAN	fb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1312	11218	21075	5.18	4.0E-06	A1334928.1	EST_HUMAN	fb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1458	11363	21227	2.23	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2218	12104	22008	1.22	4.0E-06	AW015401.1	EST_HUMAN	UIH-B10-aat-f05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3025	12953	22746	1.39	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3819	13731	23520	1.78	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4702	14588	24378	1.58	4.0E-06	A1856399.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
4840	14721	24504	1.02	4.0E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7109	16986	27177	3.1	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRCV753A2 to TCRCV12S2 region
8746	17895	28139	3.74	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2117	12006	21904	1.27	3.0E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2117	12006	21905	1.27	3.0E-06	AA700562.1	EST_HUMAN	z134b08.s1 Soares fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2220	12105		1.37	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2891	12818	22610	0.95	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3228	13152		2.14	3.0E-06	A1857779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element ;
3716	13628	23412	1.26	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3716	13628	23413	1.26	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4376	14272	24053	0.9	3.0E-06	T50286.1	EST_HUMAN	yg78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4461	14355	24146	4.31	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6290	16154		1.92	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9494	19110		4.17	3.0E-06	AW385262.1	EST_HUMAN	RCO-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
195	10167		3.28	2.0E-06	P54396	SWISSPROT	HOMEBOX PROTEIN GOOSECOID

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1550	11455		6.27	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2326	12207	22106	2.95	2.0E-06	A1672138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element ;
2418	12295	22192	2.14	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2519	12393	22285	2.69	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3475	13391	23196	1.11	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDE05 3'
3700	13614	23398	1.5	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3710	13623	23406	1.5	2.0E-06	AB030898.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5378	15784	26904	5.08	2.0E-06	A1819424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7136	17013	27206	1.95	2.0E-06	H62051.1	EST_HUMAN	yu37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9403	19699	24901	1.35	2.0E-06	P23249	SWISSPROT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN); PROTEIN MOV-10
9548	19148		2.46	2.0E-06	BE328232.1	EST_HUMAN	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element ;
31	10018	19813	1.9	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH- AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
641	10578	20394	1.61	1.0E-06	AF084364.1	NT	Mus musculus D6MM5E protein (D6M5e) mRNA, complete cds
1435	11340	21206	2.22	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1507	11412	21271	1.09	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1554	11459	21317	0.93	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1554	11459	21318	0.93	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1555	11470	21729	1.2	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1949	11844	21729	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1949	11844	21730	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	14172	23949	11.11	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5043	14915	24688	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5043	14915	24689	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5233	15157	24925	4.69	1.0E-06	BF533015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
6107	16001	26139	6.11	1.0E-06	P02671	SWISSPROT	FBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
6813	16692	26881	1.16	1.0E-06	A1347010.1	EST_HUMAN	qb54e02.x1 NCI_CGAP_C8 Homo sapiens cDNA clone IMAGE:1926642 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	16822	27013	1.53	1.0E-06	AI287878.1	EST_HUMAN	q123f06.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
7582	17433	27647	3.72	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7582	17433	27648	3.72	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7609	17460	27676	4.86	1.0E-06	AA132611.1	EST_HUMAN	zo17e08.r1 Stratagene clone (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
7637	17488		3.73	1.0E-06	AA449257.1	EST_HUMAN	zx04d11.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
7989	17639		1.52	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8912	18720		4.81	1.0E-06	AW890841.1	EST_HUMAN	RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA
9440	19077	25280	2.99	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
9536	11844	21729	1.84	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
9536	11844	21730	1.84	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
357	10314	20134	1.49	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
357	10314	20135	1.49	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8572	18440	28708	2.38	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4661	14547	24336	4.49	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4661	14547	24337	4.49	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5589	15504		7.45	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
6667	16547		7.89	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8993	18703		7.2	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
9055	18838		4.15	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1822	11719	21599	0.94	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
1870	11766	21641	2.36	6.0E-07	AW855558.1	EST_HUMAN	CM3-C10277-221039-024-e11 CT0277 Homo sapiens cDNA
2442	12319	22217	2.41	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
3891	13802		1.65	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
7279	17156	27351	1.35	6.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L.;
9303	19653		1.81	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
323	10284		3.55	5.0E-07	AI631893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1041	10969		2.9	5.0E-07	AA380630.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
2995	12923		0.87	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4547	14440	24223	1.44	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6203	15963	26096	1.71	5.0E-07	AI393981.1	EST_HUMAN	ig06b05.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element
6203	15963	26097	1.71	5.0E-07	AI393981.1	EST_HUMAN	ig06b05.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element
6348	16211	26373	15.93	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCL CGAP_Br18 Homo sapiens cDNA clone IMAGE:2668362 3' similar to gb:X15341
7932	17782	28021	4.11	5.0E-07	AI908587.1	EST_HUMAN	CYTOKROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8805	18619	28909	4.31	5.0E-07	P11087	SWISSPROT	GM-BT178-220499-014 BT178 Homo sapiens cDNA
8863	18675		2.06	5.0E-07	AJ271735.1	NT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
9712	19556		2.02	5.0E-07	AW852537.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3918	13827	23608	1.98	4.0E-07	AW009602.1	EST_HUMAN	GV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
7235	17112	27305	5.29	4.0E-07	AW419134.1	EST_HUMAN	ws84h05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
8308	18185	28432	3.84	4.0E-07	AJ765528.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2866548 3'
8308	18185	28433	3.84	4.0E-07	AJ765528.1	EST_HUMAN	wi81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
8552	18422		2.05	4.0E-07	BE001828.1	EST_HUMAN	wi81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
434	10379	20200	5.01	3.0E-07	U19719.1	NT	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
568	10507	20314	2.38	3.0E-07	AJ271735.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
1352	11258	21114	2.19	3.0E-07	M99149.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1608	11513		2.23	3.0E-07	M64857.1	NT	Human polymorphic microsatellite DNA
2000	11893		1.01	3.0E-07	AA526763.1	EST_HUMAN	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2242	12126	22026	1.15	3.0E-07	M99149.1	NT	nif6b09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element
2420	12297	22194	17.25	3.0E-07	BE005077.1	EST_HUMAN	Human polymorphic microsatellite DNA
2420	12297	22195	17.25	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2998	12926	22718	0.85	3.0E-07	T84704.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3122	13047	22844	1.82	3.0E-07	P38739	SWISSPROT	yd50f12.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:111695 5'
4624	14512	24302	7.05	3.0E-07	AV650201.1	EST_HUMAN	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4654	14540	24328	0.89	3.0E-07	AJ797236.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4996	14871	24634	1.47	3.0E-07	T57850.1	EST_HUMAN	we86b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
4996	14871	24635	1.47	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
							yc14h09.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5476	15396	25462	10.28	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6026	15930		5.32	3.0E-07	AA815175.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6433	16294	26456	3	3.0E-07	AW797168.1	EST_HUMAN	cc04c10.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338890 3'
							QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
8918	18726		3	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9939	19408		2.76	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
26	10013	19807	2.62	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP-1) mRNA, complete cds
148	10122	19940	4.75	2.0E-07	L77689.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
148	10122	19941	4.75	2.0E-07	L77689.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
175	10146	19952	116.1	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	10663	20495	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	10663	20496	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650859 3' similar to gb:U31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
928	10853	20701	3.11	2.0E-07	AA223260.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
929	10854	20702	3.38	2.0E-07	T63042.1	EST_HUMAN	I/6 AUTOANTIGEN
1147	11060	20903	1.28	2.0E-07	Q26788	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
1592	11486	21347	1.84	2.0E-07	Q09701	SWISSPROT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
3633	13547	23334	14.74	2.0E-07	AF125348.1	NT	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
							CE00923 PROBABLE RABGAP DOMAINS ;
5078	14948	24723	0.97	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
							CE00923 PROBABLE RABGAP DOMAINS ;
5078	14948	24724	0.97	2.0E-07	AW070995.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
5198	15061	24826	0.95	2.0E-07	AL163301.2	NT	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
5277	15199	24975	1.73	2.0E-07	AW898066.1	EST_HUMAN	gg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6009	15914	26041	1.69	2.0E-07	AI208715.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
6934	16812		3.91	2.0E-07	AV729390.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7627	17478		1.61	2.0E-07	AL163303.2	NT	CMA-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA
7891	17741	27984	6.48	2.0E-07	AW892507.1	EST_HUMAN	zr85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
9094	19557		1.48	2.0E-07	AF732462.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
1086	11002		1.21	1.0E-07	AL163282.2	NT	

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12280	22177	0.94	1.0E-07	7549818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2797	11410	21269	1.75	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3684	11002		1.33	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4195	14095	23874	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4195	14095	23875	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6103	15997	26132	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6103	15997	26133	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6424	16285	26447	9.04	1.0E-07	N65081.1	EST_HUMAN	yy43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
6782	16661	26850	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
6782	16661	26851	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7180	17057	27246	3.24	1.0E-07	AA693576.1	EST_HUMAN	z151et10.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
7714	17564	27790	2.37	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
7716	17566	27792	1.28	1.0E-07	AA386311.1	EST_HUMAN	EST186054 Brain IV Homo sapiens cDNA
7980	17830		1.56	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9364	19633	25060	3.66	1.0E-07	BE048770.1	EST_HUMAN	h153c11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
9497	19113		1.37	1.0E-07	X64467.1	NT	DJ1163J1.1;
9661	19222		4.61	1.0E-07	X51755.1	NT	H.sapiens ALAD gene for porphobilinogen synthase
7689	17539	27765	1.67	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
8520	18392	28656	2.91	9.0E-08	AB91052.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cBABFB06 5'
8922	18730	28025	3.91	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
9316	19008		3.09	9.0E-08	AJ251973.1	NT	OFR repetitive element;
591	12671		2.65	8.0E-08	AB911352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1034	10952		0.88	8.0E-08	BE794469.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
3498	13415		1.43	8.0E-08	BE795469.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
7074	16951	27144	3.38	8.0E-08	AF52367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7074	16951	27145	3.38	8.0E-08	AF52367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7551	17402	27616	2.89	8.0E-08	AW970993.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8570	18438		2.39	8.0E-08	AF253417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
							EST1382776 IMAGE resequences, MAGK Homo sapiens cDNA
							Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
73	10057	19874	3.27	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1338	11244	21102	12.71	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3528	13444	29240	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	13444	29241	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8189	18075		4.63	7.0E-08	A1535743.1	EST_HUMAN	cong5.P11.A5 conorm Homo sapiens cDNA 3'
8926	18734	29027	5.6	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
9770	13444	29240	4.54	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9770	13444	29241	4.54	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9834	19334		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
800	10729	20569	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10729	20570	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12193	22092	1.73	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
4155	14055	23829	0.99	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8717	18534	28818	2.26	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8819	18632		1.74	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
79	10063	19880	3.06	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	12076	21981	1.97	5.0E-08	AA493851.1	EST_HUMAN	nt03b09.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
5178	15042	24809	1.12	5.0E-08	Q06278	SWISSPROT	ALDEHYDE OXIDASE
9057	18859		4.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
9245	18958	26317	1.94	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1724	11625	21493	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21494	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
7278	17155	27350	1.41	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
7938	17798	28030	4.17	4.0E-08	A050027.1	EST_HUMAN	an22a10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
8274	18154		1.79	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
8499	18313	28570	3.66	4.0E-08	BF592493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
8499	18313	28571	3.66	4.0E-08	BF592493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
9061	19680		1.54	4.0E-08	W76159.1	EST_HUMAN	zd65g03.r1 Soares_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:346566 5' similar to contains L1.t1 L1 repetitive element ;
9703	19252		1.46	4.0E-08	A343353.1	EST_HUMAN	tb95a11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5184	15048	24812	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5184	15048	24813	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5446	15367	25423	1.99	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
6163	15120	24864	3.58	3.0E-08	AI792737.1	EST_HUMAN	SYNTAXIN 17.1
6451	16312	26478	1.41	3.0E-08	AL163246.2	NT	qs76f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
							Homo sapiens chromosome 21 segment HS21C046
6558	16416		2.97	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9027	18819		11.6	3.0E-08	R18420.1	EST_HUMAN	yg02f04.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
199	10171		15.76	2.0E-08	AW302996.1	EST_HUMAN	xr87f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
223	10194		7.97	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares fetal_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
488	10431	20245	1.48	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
644	10581	20396	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
644	10581	20397	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
974	10898		37.42	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1319	11226	21082	1.93	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1707	11608		1.03	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1811	11708		3.99	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2368	12248	22140	1.42	2.0E-08	AA731948.1	EST_HUMAN	hw64h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.t3 L1 repetitive element ;
2496	12371		2.16	2.0E-08	K00216.1	NT	Sheep His-tRNA-GUG
3171	13096	22901	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3171	13096	22902	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3783	13695		1.66	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
3986	13893	23669	0.78	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4305	14203		3.35	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 repetitive element ;
4876	14756		2.89	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element;
6722	16802	26791	1.31	2.0E-08	AA490121.1	EST_HUMAN	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8995	18799	29092	11.62	2.0E-08	BF569904.1	EST_HUMAN	nea32a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3257969 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1493	12686	21257	1.13	1.0E-08	P31792	SWISSPROT	POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE, ENDONUCLEASE]
2005	11897		2.92	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-160999-001-f12 HT0130 Homo sapiens cDNA
3155	13080	22881	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3155	13080	22882	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5191	15054	24818	1.43	1.0E-08	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5438	15358	25414	4.05	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
6975	16852	27045	1.84	1.0E-08	AJ015304.1	EST_HUMAN	cd35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
8633	18498	28773	3.66	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
9434	19074		2.01	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9804	19316		6.3	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9894	19518		1.76	1.0E-08	BF375398.1	EST_HUMAN	MIR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4149	14049	23823	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4149	14049	23824	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3444	13361		1.07	8.0E-09	BE012076.1	EST_HUMAN	RC5-BN1058-270400-031-C06 BN1058 Homo sapiens cDNA
6307	16171	26328	6.12	8.0E-09	AJ183500.1	EST_HUMAN	qd42e07.x1 Soares_fetal_heart_Nb-H19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.1; MSR1 repetitive element ;
6666	16546	26743	2.71	8.0E-09	AW900159.1	EST_HUMAN	CMD-NM1004-100300-273-e06 NN1004 Homo sapiens cDNA
7196	17073		3.06	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1882875 3'
3555	13469		1.88	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4558	14450	24236	0.99	7.0E-09	D00649.1	NT	Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3
7335	17203	27403	3.27	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
7850	17700	27945	1.84	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
2107	11996		1.06	6.0E-09	AL040499.1	EST_HUMAN	DKFZp434C0514.1_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
3941	13849	23625	1.06	6.0E-09	AA557940.1	EST_HUMAN	nl17a11.s1 NCL_OGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ;
4906	14786	24562	4.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-H05 HT0527 Homo sapiens cDNA
5305	15226	25030	8.19	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
7294	17170	27370	2.26	6.0E-09		NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7896	17746		4.06	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1394	11299	21157	3.09	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5658	15764	28881	1.92	5.0E-09	AA359454.1	EST_HUMAN	EST068746 Fetal lung II Homo sapiens cDNA 5' end
7811	17661	27901	2.69	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
510	10452		1.68	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
949	10873		2.31	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1453	11358	21222	0.96	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2379	12259	22151	6.36	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2303	12184	22082	3.82	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2506	12380	22270	1.25	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2614	12482	22371	1.1	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3287	13208	23008	1.1	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
4329	14226	24008	3.22	3.0E-09	AF175325.1	NT	MER18 repetitive element;
4411	14305	24088	1.54	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
7884	17734	27978	1.73	3.0E-09	AL163247.2	NT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
8384	18261	28510	3.8	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
8384	18261	28511	3.8	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
795	10724		0.93	2.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1237	11144	20895	5.23	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1637	11641		10.52	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2278	12162	22059	2.25	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
3868	13769	23561	3.66	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6405	16266	26428	8.9	2.0E-09	AA461430.1	EST_HUMAN	z63h06.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7055	16932	27122	1.37	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8589	18457	28726	2.11	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9576	10724		11.53	2.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
9640	19749		1.62	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1093	11009	20850	2.48	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1093	11009	20851	2.48	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616	11520		0.95	1.0E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2453	12330		0.94	1.0E-09	AI356086.1	EST_HUMAN	qy64e11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element ;
2860	12788	22580	1.51	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2895	12822	22614	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2895	12822	22615	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2949	12876	22674	1.23	1.0E-09	P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]
3002	12930	22722	0.78	1.0E-09	BE535440.1	EST_HUMAN	801058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4692	14578		4.26	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
5560	15476	25549	1.37	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
5736	15644	25749	3.21	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7911	17761		3.1	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9478	19689	24996	2.14	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1287	11195	21048	1.8	9.0E-10	AW567740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2803	12733	22532	6.03	9.0E-10	AIB70071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
6087	16032	26172	4.63	9.0E-10	AI452982.1	EST_HUMAN	tr46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P150. ;
141	10115	19935	9.43	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	23022	0.87	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4106	14006	23782	2.82	8.0E-10	AA376832.1	EST_HUMAN	EST89664 Small intestine 1 Homo sapiens cDNA 5' end
7725	17575		2.32	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
9005	18808	29100	2.31	8.0E-10	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
686	10619	20444	12.45	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
686	10619	20445	12.46	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1605	11510	21371	1.87	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1974	11867		1.01	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2612	12386		16.88	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	12978	22768	2.65	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
5754	15662	25769	3.98	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
6514	16373		1.39	7.0E-10	P35094	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
895	10821	20866	2.81	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	6.0E-10	A424405.1	EST_HUMAN	h02d07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2096021 3'
4634	14522		2.51	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
9092	18865		1.79	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
9947	19597		3.54	6.0E-10	BE699410.1	EST_HUMAN	RC3-NN0070-110800-014-h07 NN0070 Homo sapiens cDNA
744	10675		4.5	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N219 5'
3430	13347	23152	1.48	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
6334	16197		1.82	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7496	17366	27570	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
7496	17366	27571	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
106	10087		0.99	4.0E-10	A1221083.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2NbpP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
1951	11846	21732	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2527	12401	22292	6.09	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6259	16125	26278	19.23	4.0E-10	AF224669.1	NT	Homo sapiens ribonuclease, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8436	18310		7.7	4.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
897	10822	20868	1.72	3.0E-10	N36113.1	EST_HUMAN	y32f06.s1 Soares_melanocyte 2NbpH Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element ;
1329	11236		6.63	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4435	14330	24117	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4435	14330	24118	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7595	15672	25779	2.83	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
5833	15739	25851	3.27	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
6562	16420	26599	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
6562	16420	26600	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7067	16944	27136	1.58	3.0E-10	HB7208.1	EST_HUMAN	ys74b12.s1 Soares_reitna N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ;
7233	17110	27302	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7233	17110	27303	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7979	17829		2.56	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Stratagene_lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8026	17876		1.54	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1289908 3'
9737	19271	25227	2.03	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
32	10019	19814	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
32	10019	19815	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1855	11751		5.91	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
5547	15463		2.41	2.0E-10	Q28640	SWISSPROT	(HPRG)
5787	15693	25801	1.71	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6367	16230	26389	5.79	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
1492	11397		3.56	1.0E-10	BE791082.1	EST_HUMAN	MRO-SN0036-290300-001-f01 SN0038 Homo sapiens cDNA
1589	11493	21353	3.14	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2537	12411		2.4	1.0E-10	AW852001.1	EST_HUMAN	QV0-GT0225-191199-058-e08 GT0225 Homo sapiens cDNA
3456	13372	23178	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-r1 434 (synonym: hies3) Homo sapiens cDNA
3770	13411		0.91	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3933	13842		5.44	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4036	13939	23716	4.51	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4036	13939	23717	4.51	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4042	13945	23724	2.25	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4079	13961		2.06	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5145	15012		0.93	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
7859	17709		4.59	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stralagene neuroepithelium NT2FRAM 937234 Homo sapiens cDNA clone IMAGE:548314 5'
8286	18165	28408	3.4	1.0E-10	A038280.1	EST_HUMAN	oy85h03.x1 Scores_fetal_liver_spleen_1NF1LS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
9037	15012		1.43	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
9084	18859		1.3	1.0E-10	AA397885.1	EST_HUMAN	z86p10.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:729211 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit: BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
261	10226	20042	1.2	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2057	11947	21843	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2057	11947	21844	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23064	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23065	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4400	14295	24079	1.09	9.0E-11	AA775985.1	EST_HUMAN	ae7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5421	15342		4	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
9410	19062	25312	2.69	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN:506B08 5'
3078	13005		9.97	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
3881	13792	23580	0.83	8.0E-11	A1478617.1	EST_HUMAN	fm54c09.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3957	13805	23641	4.03	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1431	11336	21202	2.11	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
6949	16827	27020	2.55	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7873	17723		1.22	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9545	19145		1.31	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBAEC09 5'
406	10352	20180	5.16	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
406	10352	20181	5.16	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6529	16388	26568	3.58	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6871	16750	26945	6.49	6.0E-11	AV727856.1	EST_HUMAN	AV727856 HTC Homo sapiens cDNA clone HTCAS06 5'
11	9997	19786	0.92	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3320	9997	19788	1.48	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4135	14035	23811	1.49	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5926	15831	25954	1.69	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
6446	16307	26472	14.59	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8975	18780	26072	1.79	5.0E-11	A1269880.1	NT	Homo sapiens KIAA0351 gene (partial), X73 gene and LZTFL1 gene
1360	11285		1.4	4.0E-11	AA436042.1	EST_HUMAN	zu07b12.r1 Soares tests_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2760	12622	22514	8.45	4.0E-11	BE888900.1	EST_HUMAN	601507531.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
4518	14411	24196	1.37	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5997	15803	25927	2.94	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6362	16225		3.66	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7405	17272		1.59	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-f08 HT0256 Homo sapiens cDNA

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9611	19190	25252	1.93	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1476	11381	21245	2.15	3.0E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4179	14079		1.45	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
944	10869	20716	1.58	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1168	11080	20926	3.64	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1168	11080	20927	3.64	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1596	11500	21359	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1596	11500	21360	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1600	11505	21365	1.04	2.0E-11	AI126371.1	EST_HUMAN	gc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.1
2737	12599	22493	1.11	2.0E-11	AF087913.1	NT	L1 repetitive element;
3160	13085	22889	4.23	2.0E-11	P10263	SWISSPROT	Human endogenous retrovirus HERV-P-T47D
3284	13205	23005	0.87	2.0E-11	AI478617.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3452	13368		0.95	2.0E-11	AF020503.1	NT	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161636 3'
4501	14395		0.97	2.0E-11	AL163227.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4851	14732		5.46	2.0E-11	BE062558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
4861	14836	24604	1.32	2.0E-11	AA307331.1	EST_HUMAN	QV2-BT0258-261039-014-a01 BT0258 Homo sapiens cDNA
5810	15715	25828	1.83	2.0E-11	AA581028.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin
7318	17194		1.43	2.0E-11	AF029308.1	NT	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7900	17750	27989	4.61	2.0E-11	Q13606	SWISSPROT	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.;
8457	18330	28591	2.07	2.0E-11	AA033369.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
8457	18330	28592	2.07	2.0E-11	AA033369.1	EST_HUMAN	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
9160	19679		1.29	2.0E-11	AA704195.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
9192	18927		2.25	2.0E-11	AW842143.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
9216	18943	25356	1.98	2.0E-11	BF377859.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9477	19103		1.89	2.0E-11	D25217.2	NT	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
							CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA0027 protein, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	19201		2.38	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9930	19401		2.38	2.0E-11	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
860	10594	20412	1.24	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1199	11109	20954	2.58	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1483	11388		1.94	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2079	11969	21862	3.12	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3454	13370	23174	1.32	1.0E-11	BE004315.1	EST_HUMAN	CMO-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5269	15191	24966	14.34	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6773	16852	26840	3.25	1.0E-11	4885548	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
6989	16866	27060	5.41	1.0E-11	R13174.1	EST_HUMAN	y73d08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166 5'
7232	17109	27300	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
7232	17109	27301	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
8607	18474	28747	1.9	1.0E-11	BF680078.1	EST_HUMAN	602154807F-1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
9702	19483		1.29	1.0E-11	Z20377.1	EST_HUMAN	HSAACACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
2822	12849	22649	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
7641	17491	27712	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7641	17491	27713	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9270	18974		3.57	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4562	14454	24241	2.75	7.0E-12	Q05904	SWISSPROT	34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)
8956	18545	28828	11.23	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3500	13417		0.92	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWf06 5'
4252	14151	23925	7.85	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
7201	17078	27263	1.19	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
7453	17262		1.86	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1027	10945	20790	2.88	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element
3344	13264	23070	1.18	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33
3666	13580	23367	5.93	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCI_CGAP_Brm62 Homo sapiens cDNA clone IMAGE:2281217 5'
5171	15037		0.84	5.0E-12	AA720661.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
5667	15578	25676	4.75	5.0E-12	AL163278.2	NT	mw24b11.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241373 3'
5667	15578	25677	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5909	15815	25940	9.12	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7268	17145	27339	2.15	5.0E-12	AJ271735.1	NT	EST136850 IMAGE ressequences, MAGN Homo sapiens cDNA
							Homo sapiens Xq pseudautosomal region; segment 1/2

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7895	17745		4.67	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
244	10211	20027	3.42	4.0E-12	AA700326.1	EST_HUMAN	2174g11.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	10211	20027	3.55	4.0E-12	AA700326.1	EST_HUMAN	2174g11.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4620	14413	24198	0.85	4.0E-12	A1689984.1	EST_HUMAN	3c26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
6797	16676		2.89	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8431	18305	28561	3.51	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9520	19131		1.9	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
900	10536	20345	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
900	10536	20345	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
8047	17938	28187	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
8047	17938	28188	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3421	13338	23143	1.03	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4025	13928	23704	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4025	13928	23705	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4324	14221		1.8	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	14688	24473	0.78	2.0E-12	O70306	SWISSPROT	TXB15 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12	O70306	SWISSPROT	TXB15 PROTEIN (T-BOX PROTEIN 15)
5898	15804		2.22	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
6258	16124	26277	3.34	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
6516	16375	26552	2.07	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7367	17345		1.68	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7737	17587		8.13	2.0E-12	BE163980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9175	18916		1.71	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9377	19041		1.52	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
117	10095	19914	1.82	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element;
1944	11839		2.03	1.0E-12	A1871726.1	EST_HUMAN	wm51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element;
3032	12980	22752	1.16	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds